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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:21:47 ; Search time 29 Seconds
(without alignments)
10.296 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 12390

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	1	US-08-002-202-10
2	21	100.0	4	3	US-08-481-534-10
3	21	100.0	4	3	US-08-481-534-15
4	16	76.2	4	1	US-08-021-608D-22
5	16	76.2	4	1	US-08-002-202-15
6	16	76.2	4	1	US-08-726-160-22
7	16	76.2	4	2	US-08-685-589A-27
8	16	76.2	4	2	US-08-685-589A-28
9	16	76.2	4	2	US-08-685-589A-29
10	16	76.2	4	3	US-09-400-208B-8
11	16	76.2	4	3	US-09-400-208B-12
12	16	76.2	4	4	US-09-417-608A-88
13	16	76.2	4	4	US-09-400-122A-8
14	16	76.2	4	4	US-09-400-122A-12
15	15	71.4	3	1	US-08-221-582A-1
16	15	71.4	4	1	US-07-906-349A-16
17	15	71.4	4	1	US-08-102-757-23
18	15	71.4	4	1	US-08-167-035-16
19	15	71.4	4	1	US-08-255-272-21
20	15	71.4	4	1	US-08-208-887A-16
21	15	71.4	4	1	US-08-582-257-28
22	15	71.4	4	2	US-08-582-298-28
23	15	71.4	4	2	US-07-963-538B-8
24	15	71.4	4	2	US-08-539-005-16
25	15	71.4	4	3	US-09-320-095-11
26	15	71.4	4	3	US-09-523-487-11
27	15	71.4	4	3	US-08-811-463-37

28	15	71.4	4	3	US-09-388-183-7	Sequence 7, Appli
29	15	71.4	4	3	US-09-280-598-16	Sequence 16, Appli
30	15	71.4	4	4	US-09-933-497B-37	Sequence 37, Appli
31	15	71.4	4	6	5171670-4	Patent No. 5171670
32	15	71.4	4	6	5171670-4	Patent No. 5171670
33	14	66.7	4	1	US-08-102-896-4	Sequence 4, Appli
34	14	66.7	4	1	US-08-280-443-39	Sequence 39, Appli
35	14	66.7	4	1	US-08-457-453-39	Sequence 39, Appli
36	14	66.7	4	1	US-08-555-678-39	Sequence 39, Appli
37	14	66.7	4	1	US-08-478-913-3	Sequence 3, Appli
38	14	66.7	4	2	US-08-685-589A-4	Sequence 4, Appli
39	14	66.7	4	4	US-09-480-718-48	Sequence 48, Appli
40	14	66.7	4	4	US-09-211-715-175	Sequence 175, App
41	14	66.7	4	4	US-09-211-715-176	Sequence 176, App
42	14	66.7	4	4	US-09-211-715-177	Sequence 177, App
43	14	66.7	4	4	US-09-211-715-178	Sequence 178, App
44	14	66.7	4	5	PCT-US95-02275-39	Sequence 39, Appli
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47	13	61.9	4	1	US-08-260-199A-30	Sequence 30, Appli
48	13	61.9	4	3	US-08-757-177-1	Sequence 1, Appli
49	13	61.9	4	3	US-08-927-128-10	Sequence 10, Appli
50	13	61.9	4	3	US-08-974-549A-69	Sequence 69, Appli
51	13	61.9	4	4	US-08-912-951-69	Sequence 69, Appli
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53	13	61.9	4	4	US-09-721-456-69	Sequence 69, Appli
54	13	61.9	4	4	US-09-784-642-10	Sequence 10, Appli
55	13	61.9	4	4	US-08-278-774-5	Sequence 5, Appli
56	13	61.9	4	5	PCT-US93-06591-4	Sequence 4, Appli
57	12	57.1	3	1	US-07-816-679A-8	Sequence 8, Appli
58	12	57.1	3	1	US-07-816-679A-9	Sequence 9, Appli
59	12	57.1	3	1	US-08-365-759-1	Sequence 1, Appli
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61	12	57.1	3	1	US-08-502-989-6	Sequence 6, Appli
62	12	57.1	3	2	US-08-476-014-8	Sequence 8, Appli
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79	12	57.1	4	1	US-08-127-351-50	Sequence 50, Appli
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85	12	57.1	4	1	US-08-365-759-2	Sequence 2, Appli
86	12	57.1	4	1	US-08-365-759-4	Sequence 4, Appli
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88	12	57.1	4	1	US-08-202-178-9	Sequence 9, Appli
89	12	57.1	4	1	US-08-049-195A-3	Sequence 3, Appli
90	12	57.1	4	1	US-08-480-367B-44	Sequence 44, Appli
91	12	57.1	4	1	US-08-480-367B-50	Sequence 50, Appli
92	12	57.1	4	1	US-08-076-092-50	Sequence 50, Appli
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95	12	57.1	4	1	US-08-487-221A-44	Sequence 44, Appli
96	12	57.1	4	1	US-08-487-221A-50	Sequence 50, Appli
97	12	57.1	4	1	US-08-475-827A-1	Sequence 1, Appli
98	12	57.1	4	1	US-08-480-370-44	Sequence 44, Appli
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ALIGNMENTS

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RESULT 1
US-08-002-202-10
; Sequence 10, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-002-202-10
Query Match 100.0%; Score 21; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db 1 R1PR 4

RESULT 2
US-08-481-534-10
; Sequence 10, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-481-534-10
Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db 1 R1PR 4

RESULT 3
US-08-481-534-15
; Sequence 15, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
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REFERENCE/DOCKET NUMBER: 92,448-D
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-534-15

Query Match 100.0%; Score 21; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IPR 4

Db 1 IPR 4

RESULT 4

US-08-021-608D-22
Sequence 22, Application US/08021608D
Patent No. 5580760
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,608D

FILING DATE: 22-FEB-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WILLIAM S. FEILER

REGISTRATION NUMBER: 26,728

REFERENCE/DOCKET NUMBER: 2026-4063

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 4

TYPE: Amino Acid

STRANDEDNESS: Single

TOPOLOGY: Unknown

MOLECULE TYPE: Peptide/Protein

FEATURE:

OTHER INFORMATION: Mutant 6

US-08-021-608D-22

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4

Db 2 IPR 4

RESULT 5

US-08-002-202-15
Sequence 15, Application US/08002202
Patent No. 5604201
GENERAL INFORMATION:
APPLICANT: Thomas, Garry
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Haylick, Joel S
TITLE OF INVENTION: Methods and Reagents for Inhibiting
TITLE OF INVENTION: Furin Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:

ADDRESSEE: Allegratti and Witcoff, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/002,202

FILING DATE: 08-JAN-1993

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: No. 5604201nan, Kevin E

REGISTRATION NUMBER: 35,30003

REFERENCE/DOCKET NUMBER: 92,448

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 4 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-002-202-15

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4

Db 2 IPR 4

RESULT 6

US-08-726-160-22
Sequence 22, Application US/08726160
Patent No. 5734016
GENERAL INFORMATION:
APPLICANT: LEVENS, DAVID L., DUNCAN,
APPLICANT: ROBERT C., AND AVIGAN, MARK I.
TITLE OF INVENTION: NOVEL FUSE BINDING
TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK

[illegible]

; TOPOLOGY: No. 5916872 Relevant
; MOLECULE TYPE: Peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-28

Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 1 RIP 3

RESULT 9
US-08-685-589A-29
; Sequence 29, Application US/08685589A
; Patent No. 5916872
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 222
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,589A
; FILING DATE: 24-JUL-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: No. 5916872 Relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"

Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3

Db 1 RIP 3

RESULT 10
US-09-400-208B-8
; Sequence 8, Application US/09400208B
; Patent No. 6271011
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; PRIOR FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligopeptide
US-09-400-208B-8

Query Match 76.2%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 2 RIP 4

RESULT 11
US-09-400-208B-12
; Sequence 12, Application US/09400208B
; Patent No. 6271011
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; FILE REFERENCE: 77-96B
; CURRENT APPLICATION NUMBER: US/09/400,208B
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide motif
; OTHER INFORMATION: in Pasteurella multocida neuraminidase
US-09-400-208B-12

Query Match 76.2%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db |||
2 RIP 4

RESULT 12

US-09-417-608A-88
; Sequence 88, Application US/09417608A
; Patent No. 6686164
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/09/417,608A
; CURRENT FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 88
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-417-608A-88

Query Match 76.2%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1PR 4
Db |||
1 R1PR 4

RESULT 13

US-09-400-122A-8
; Sequence 8, Application US/09400122A
; Patent No. 6767713
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraaminidase Coding Sequences,
; FILE REFERENCE: 77-96A
; CURRENT APPLICATION NUMBER: US/09/400,122A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligopeptide
US-09-400-122A-8

Query Match 76.2%; Score 16; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 14

US-09-400-122A-12
; Sequence 12, Application US/09400122A
; Patent No. 6767713
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraaminidase Coding Sequences,
; FILE REFERENCE: 77-96A
; CURRENT APPLICATION NUMBER: US/09/400,122A
; CURRENT FILING DATE: 1999-09-21
; PRIOR APPLICATION NUMBER: US 08/951,984
; PRIOR FILING DATE: 1997-10-15
; PRIOR APPLICATION NUMBER: US 60/028,876
; PRIOR FILING DATE: 1996-10-16
; PRIOR APPLICATION NUMBER: US 60/028,482
; PRIOR FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide motif
; OTHER INFORMATION: in Pasteurella multocida neuraaminidase
US-09-400-122A-12

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 1, Application US/08221582A
; Patent No. 5505946
; GENERAL INFORMATION:
; APPLICANT: Ann R. Kennedy, Bernard F. Szuha
; TITLE OF INVENTION: Bowman-Birk Inhibitor Concentrate
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Pre-Malignant Tis
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jane Massey Licata, Esq.
; STREET: 210 Lake Drive East, Suite 201
; CITY: Cherry Hill
; STATE: NJ
; COUNTRY: USA
; ZIP: 08002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 486
; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,582A
; FILING DATE: April 1, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: 07/973,335
; APPLICATION NUMBER: No. 5505946member 2, 1992
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Jane Massey Licata
; REGISTRATION NUMBER: 32,257
; REFERENCE/DOCKET NUMBER: UPSC-0027
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 779-2400
; TELEFAX: (609) 779-8488
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3
; TYPE: amino acid
; TOPOLOGY: linear
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US-08-221-582A-1

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Best Local Similarity 66.7%; Pred. No. 4.1e+05;
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Db 1 VPR 3

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1P4

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Searched: 1714042 seqs, 383979560 residues

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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	16	76.2	4	15	US-10-601-953-4
5	16	76.2	4	16	US-10-322-266-4
6	16	76.2	4	16	US-10-311-858B-3
7	16	76.2	4	16	US-10-311-858B-11
8	16	76.2	4	16	US-10-730-454-88
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10	15	71.4	4	9	US-09-778-885-11
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18	15	71.4	4	15	US-10-601-953-212
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24	14	66.7	4	9	US-09-977-831-12
25	14	66.7	4	10	US-09-882-781-12
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ALIGNMENTS

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; Publication No. US20040127396A1
; GENERAL INFORMATION:
; APPLICANT: DUROIS, Claire
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885,914B
; PRIOR FILING DATE: 2001-06-22
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Variant of Homo sapiens alphan-antitrypsin reactive site
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1)
; OTHER INFORMATION: Ala355 to Arg355 variant of reactive site of alphan-antitrypsin
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; NAME/KEY: MUTAGEN
; LOCATION: (4)..(4)
; OTHER INFORMATION: Met358 to Arg358 variant of reactive site of alphan-antitrypsin
US-09-885-914B-2

Query Match 100.0%; Score 21; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
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RESULT 2
US-09-400-122-8
; Sequence 8, Application US/09400122
; Publication No. US20040072153A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
; TITLE OF INVENTION: Compositions and Diagnostic Methods

; FILE REFERENCE: 77-96a
; CURRENT APPLICATION NUMBER: US/09/400,122
; CURRENT FILING DATE: 1999-09-21
; EARLIER APPLICATION NUMBER: US 08/951,984
; EARLIER FILING DATE: 1997-10-15
; EARLIER APPLICATION NUMBER: USV 60/028,876
; EARLIER FILING DATE: 1996-10-16
; EARLIER APPLICATION NUMBER: US 60/028,482
; EARLIER FILING DATE: 1996-10-15
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligopeptide
; OTHER INFORMATION: sequence
US-09-400-122-8

Query Match 76.2%; Score 16; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-10-462-452-4
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; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-0205
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-4

Query Match 76.2%; Score 16; DB 15; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 4, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; TITLE OF INVENTION: Therapeutic Compounds
; FILE REFERENCE: 02-0305
; CURRENT APPLICATION NUMBER: US/10/601,953

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; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-4

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 2 RIP 4

RESULT 5
US-10-322-266-4
; Sequence 4, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; FILE REFERENCE: NPC10567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-4

Query Match
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QY 1 RIP 3
Db 2 RIP 4

RESULT 6
US-10-311-858B-3
; Sequence 3, Application US/10311858B
; Publication No. US20040116656A1
; GENERAL INFORMATION:
; APPLICANT: DU, Yucang
; APPLICANT: SHEN, Jinhuan
; TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
; FILE REFERENCE: SHA 110
; CURRENT APPLICATION NUMBER: US/10/311,858B
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: PCT/CN01/00875
; PRIOR FILING DATE: 2001-05-28
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Fragments
US-10-311-858B-3

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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 2 RIP 4

RESULT 7
US-10-311-858B-11
; Sequence 11, Application US/10311858B
; Publication No. US20040116656A1
; GENERAL INFORMATION:
; APPLICANT: DU, Yucang
; APPLICANT: SHEN, Jinhuan
; TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
; FILE REFERENCE: SHA 110
; CURRENT APPLICATION NUMBER: US/10/311,858B
; CURRENT FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: PCT/CN01/00875
; PRIOR FILING DATE: 2001-05-28
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 11
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; OTHER INFORMATION: Peptide Fragments
US-10-311-858B-11

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QY 2 IPR 4
Db 2 IPR 4

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US-10-730-454-88
; Sequence 88, Application US/10730454
; Publication No. US20040175757A1
; GENERAL INFORMATION:
; APPLICANT: Olsen, Arne
; APPLICANT: Roggen, Erwin
; APPLICANT: Ernst, Steffen
; TITLE OF INVENTION: Low Allergenic Protein Variants
; FILE REFERENCE: 5676.200-US
; CURRENT APPLICATION NUMBER: US/10/730,454
; CURRENT FILING DATE: 2003-12-08
; PRIOR APPLICATION NUMBER: US/09/417,608
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 101
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; SEQ ID NO 88
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-730-454-88

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RESULT 9
US-10-745-733-43
; Sequence 43, Application US/10745733
; Publication No. US20040259113A1
; GENERAL INFORMATION:
; APPLICANT: Tindall, D.J.
; APPLICANT: Young, C.Y.F.
; APPLICANT: McCormick, D.J.
; APPLICANT: Klee, G.G.
; APPLICANT: Saedi, M.S.
; APPLICANT: Kumar, A.
; APPLICANT: Rittenhouse, H.G.
; APPLICANT: Wolfert, R.L.
; TITLE OF INVENTION: Method for detection of metastatic prostate cancer
; FILE REFERENCE: 545.005U1
; CURRENT APPLICATION NUMBER: US/10/745,733
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US/08/759,354
; PRIOR FILING DATE: 1996-11-14
; PRIOR APPLICATION NUMBER: PCT/US96/06167
; PRIOR FILING DATE: 1996-05-02
; PRIOR APPLICATION NUMBER: US 08/622,046
; PRIOR FILING DATE: 1996-03-26
; PRIOR APPLICATION NUMBER: US 08/427,767
; PRIOR FILING DATE: 1995-05-02
; PRIOR APPLICATION NUMBER: US 08/241,174
; PRIOR FILING DATE: 1994-05-10
; PRIOR APPLICATION NUMBER: US 08/096,946
; PRIOR FILING DATE: 1993-07-22
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-745-733-43

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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db 1 RVP 3

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US-09-778-885-11
; Sequence 11, Application US/09778885
; Publication No. US20020039748A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE AND MATERIALS
; FILE REFERENCE: 98-22
; CURRENT APPLICATION NUMBER: US/09/778,885
; CURRENT FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 09/320,095
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 60/087,032
; PRIOR FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: thrombin cleavage site
US-09-778-885-11

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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
Db 2 VPR 4

RESULT 11
US-09-933-497B-37
; Sequence 37, Application US/09933497B
; Patent No. US20020098193A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Elizabeth S.
; TITLE OF INVENTION: IMMUGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
; FILE REFERENCE: UTSD:483
; CURRENT APPLICATION NUMBER: US/09/933,497B
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 60/013,563
; PRIOR FILING DATE: 1996-03-18
; NUMBER OF SEQ ID NOS: 39
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; LENGTH: 4
; TYPE: PRT
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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
Db 1 VPR 3

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US-09-819-136-6
; Sequence 6, Application US/09819136
; Patent No. US20020146789A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR
; FILE REFERENCE: 00-25
; CURRENT APPLICATION NUMBER: US/09/819,136
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/193,642
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: thrombin cleavage site
US-09-819-136-6

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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
Db 2 VPR 4

RESULT 13
US-10-021-963-7

; Sequence 7, Application US/10021963
; Publication No. US20020110887A1
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUN6
; FILE REFERENCE: 98-40
; CURRENT APPLICATION NUMBER: US/10/021,963
; CURRENT FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US/09/388,183
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Fast-Seq for Windows Version 3.0
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; LENGTH: 4
; TYPE: PRT
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US-10-021-963-7

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Db 2 VPR 4

RESULT 14
US-10-462-452-130
; Sequence 130, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 130
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; ORGANISM: Homo sapiens
US-10-462-452-130

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Db 2 RVP 4

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; Sequence 14, Application US/10301849A
; Publication No. US20040040053A1
; GENERAL INFORMATION:
; APPLICANT: Goshima, Naoki
; APPLICANT: Kisu, Yasutomo
; APPLICANT: Sono, Saki
; TITLE OF INVENTION: Method For the Preparation of Nucleic Acids
; FILE REFERENCE: 0942.5600000

; CURRENT APPLICATION NUMBER: US/10/301,849A
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: JP2001-357821
; PRIOR FILING DATE: 2001-11-22
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Thrombin cleavage site
US-10-301-849A-14

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Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
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Db 2 VPR 4

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Job time : 105 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
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Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1P4

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Total number of hits satisfying chosen parameters: 61006

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Maximum Match 100%

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3	21	100.0	4	23	US-09-885-914B-2	Sequence 2, Appl
4	16	76.2	4	1	PCT-US03-19261-4	Sequence 4, Appl
5	16	76.2	4	1	PCT-US03-19994-4	Sequence 27, Appl
6	16	76.2	4	1	PCT-US97-12974A-27	Sequence 27, Appl
7	16	76.2	4	1	PCT-US97-12974A-28	Sequence 28, Appl
8	16	76.2	4	1	PCT-US97-12974A-29	Sequence 29, Appl
9	16	76.2	4	1	PCT-US97-19557-27	Sequence 27, Appl
10	16	76.2	4	1	PCT-US97-19557-28	Sequence 28, Appl
11	16	76.2	4	1	PCT-US97-19557-29	Sequence 29, Appl
12	16	76.2	4	3	US-07-929-181B-20	Sequence 20, Appl
13	16	76.2	4	13	US-08-951-984-8	Sequence 8, Appl
14	16	76.2	4	16	US-09-290-034C-3	Sequence 3, Appl
15	16	76.2	4	16	US-09-290-034C-5	Sequence 5, Appl
16	16	76.2	4	17	US-09-340-852-27	Sequence 27, Appl
17	16	76.2	4	17	US-09-340-852-28	Sequence 28, Appl
18	16	76.2	4	17	US-09-340-852-29	Sequence 29, Appl
19	16	76.2	4	29	US-10-311-858B-3	Sequence 3, Appl
20	16	76.2	4	29	US-10-311-858B-11	Sequence 11, Appl
21	16	76.2	4	29	US-10-322-266-4	Sequence 4, Appl
22	16	76.2	4	30	US-10-462-452-4	Sequence 4, Appl
23	16	76.2	4	32	US-10-601-953-4	Sequence 4, Appl
24	16	76.2	4	33	US-10-730-454-88	Sequence 88, Appl
25	15	71.4	3	11	US-08-759-354E-43	Sequence 43, Appl
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45	15	71.4	4	23	US-09-819-136-6	Sequence 6, Appl
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ALIGNMENTS

RESULT 1
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; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-372-003-10
Query Match 100.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIPR 4
DB 1 RIPR 4
RESULT 2
US-09-372-003-15
; Sequence 15, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-372-003-15
Query Match 100.0%; Score 21; DB 17; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RIPR 4

Db 1 R1P 4
||||

RESULT 3

PCT-US03-914B-2
; Sequence 4: Application US/09885914B
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Claire
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885,914B
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variant of Homo sapiens alphan-antitrypsin reactive site
; NAME/KEY: MUTAGEN
; LOCATION: (1)..(1)
; OTHER INFORMATION: Ala355 to Arg355 variant of reactive site of alphan-antitrypsin
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (4)..(4)
; OTHER INFORMATION: Met358 to Arg358 variant of reactive site of alphan-antitrypsin
US-09-885-914B-2

Query Match 100.0%; Score 21; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R1P 4
||||

Db 1 R1P 4

RESULT 4

PCT-US03-19261-4
; Sequence 4: Application PC/TUS0319261
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02PCT
; CURRENT APPLICATION NUMBER: PCT/US03/19261
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-19261-4

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R1P 3

Db 2 R1P 4
||||

RESULT 5

PCT-US03-19994-4
; Sequence 4: Application PC/TUS0319994
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03PCT
; CURRENT APPLICATION NUMBER: PCT/US03/19994
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
PCT-US03-19994-4

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 R1P 3
||||

Db 2 R1P 4

RESULT 6

PCT-US97-12974A-27
; Sequence 27: Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: 23 Jul 97
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/685,589
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141

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; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-27

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db |||
1 RIP 3

RESULT 7
PCT-US97-12974A-28
; Sequence 28, Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: 23 Jul 97
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/685,589
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-228
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-28

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db |||
1 RIP 3

RESULT 8
PCT-US97-12974A-29
; Sequence 29, Application PC/TUS9712974A
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/12974A
; FILING DATE: 23 Jul 97
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/685,589
; FILING DATE: 24-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-026-228
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-12974A-29

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db |||
1 RIP 3

RESULT 9
PCT-US97-19557-27
; Sequence 27, Application PC/TUS9719557
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
```

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; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/19557
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-048-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-27

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIP 3
Db 1 RIP 3

RESULT 10
PCT-US97-19557-28
; Sequence 28, Application PC/TUS9719557
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/19557
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-048-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; FILING DATE: herewith
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; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-048-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-28

Query Match 76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIP 3
Db 1 RIP 3

RESULT 11
PCT-US97-19557-29
; Sequence 29, Application PC/TUS9719557
; GENERAL INFORMATION:
; APPLICANT: Chang, Conway
; APPLICANT: Gu, Leo
; APPLICANT: Chen, Jie
; TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
; NUMBER OF SEQUENCES: 241
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/19557
; FILING DATE: herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 8067-048-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
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; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-29

Query Match          76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
DB 1 RIP 3

RESULT 12
US-07-929-181B-20
; Sequence 20, Application US/07929181B
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: TETRAPEPTIDE AND METHOD OF USE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SHELDON & MAK
; STREET: 401 Florence Street, First Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch, 1.44 MB
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/929,181B
; FILING DATE: 07-AUG-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Cranfill, Raymond B
; REGISTRATION NUMBER: 32,845
; REFERENCE/DOCKET NUMBER: RATH-10007.00
; TELEPHONE: 415-322-5333
; TELEFAX: 415-322-5333
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-929-181B-20

Query Match          76.2%; Score 16; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
DB 2 IPR 4

RESULT 13
US-08-951-984-8
; Sequence 8, Application US/08951984
; GENERAL INFORMATION:
; APPLICANT: Lee, Margie
; APPLICANT: Henk, Adam
; TITLE OF INVENTION: Neutaminidase, Coding Sequences,
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder

Query Match          76.2%; Score 16; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
DB 1 RIP 3

STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,984
FILING DATE: 15-OCT-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,482
FILING DATE: 15-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,876
FILING DATE: 16-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 77-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-951-984-8

Query Match          76.2%; Score 16; DB 13; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
DB 2 RIP 4

RESULT 14
US-09-290-034C-3
; Sequence 3, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: elastase
; OTHER INFORMATION: recognition site
US-09-290-034C-3

Query Match          76.2%; Score 16; DB 16; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
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Db |||
2 IPR 4

RESULT 15
US-09-290-034C-5
; Sequence 5, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: furin
; OTHER INFORMATION: recognition sequence
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa residue can be any amino acid
US-09-290-034C-5

Query Match 76.2%; Score 16; DB 16; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RPR 4
|||
Db 1 RXPR 4

Search completed: June 20, 2005, 16:46:42
Job time : 330.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:30:17 ; Search time 37 Seconds
(without alignments)
13.327 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 583429 seqs, 123271311 residues

Total number of hits satisfying chosen parameters: 4687

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	95.2	4	6	US-10-892-402-108
2	17	81.0	4	6	US-10-892-402-144
3	16	76.2	4	6	US-10-892-402-120
4	15	71.4	3	6	US-10-529-163-28
5	15	71.4	3	6	US-10-529-163-30
6	15	71.4	4	6	US-10-892-402-11
7	15	71.4	4	6	US-10-892-402-59
8	15	71.4	4	6	US-10-892-402-100
9	15	71.4	4	6	US-10-892-402-104
10	15	71.4	4	6	US-10-123-036B-17
11	15	71.4	4	7	US-11-106-715-87
12	14	66.7	4	6	US-10-892-402-76
13	14	66.7	4	6	US-10-892-402-80
14	14	66.7	4	6	US-10-892-402-84
15	14	66.7	4	6	US-10-892-402-132
16	14	66.7	4	6	US-10-498-691A-16
17	13	61.9	3	7	US-11-138-966-679
18	13	61.9	4	6	US-10-924-367A-3
19	13	61.9	4	7	US-11-138-966-680
20	12	57.1	3	6	US-10-490-776A-331
21	12	57.1	3	6	US-10-716-095A-10
22	12	57.1	3	7	US-11-066-697-1153
23	12	57.1	4	5	US-09-931-009B-2
24	12	57.1	4	5	US-09-868-813B-6
25	12	57.1	4	6	US-10-467-657A-6678

26	12	57.1	4	6	US-10-524-157-1	Sequence 1, Appli
27	12	57.1	4	6	US-10-356-656-10	Sequence 10, Appl
28	12	57.1	4	6	US-10-356-656-13	Sequence 13, Appl
29	12	57.1	4	6	US-10-892-402-23	Sequence 23, Appl
30	12	57.1	4	6	US-10-892-402-28	Sequence 28, Appl
31	12	57.1	4	6	US-10-892-402-32	Sequence 32, Appl
32	12	57.1	4	6	US-10-892-402-35	Sequence 35, Appl
33	12	57.1	4	6	US-10-892-402-36	Sequence 36, Appl
34	12	57.1	4	6	US-10-892-402-47	Sequence 47, Appl
35	12	57.1	4	6	US-10-892-402-71	Sequence 71, Appl
36	12	57.1	4	6	US-10-892-402-83	Sequence 83, Appl
37	12	57.1	4	6	US-10-892-402-95	Sequence 95, Appl
38	12	57.1	4	6	US-10-892-402-107	Sequence 107, App
39	12	57.1	4	6	US-10-892-402-109	Sequence 109, App
40	12	57.1	4	6	US-10-892-402-126	Sequence 126, App
41	12	57.1	4	6	US-10-892-402-130	Sequence 130, App
42	12	57.1	4	6	US-10-892-402-134	Sequence 134, App
43	12	57.1	4	6	US-10-892-402-136	Sequence 136, App
44	12	57.1	4	6	US-10-892-402-140	Sequence 140, App
45	12	57.1	4	6	US-10-892-402-152	Sequence 152, App
46	12	57.1	4	6	US-10-529-115-1	Sequence 1, Appli
47	12	57.1	4	6	US-10-467-657A-6678	Sequence 6678, Ap
48	12	57.1	4	6	US-10-500-878-17	Sequence 17, Appl
49	12	57.1	4	6	US-10-684-796-314	Sequence 314, App
50	12	57.1	4	6	US-10-684-796-506	Sequence 506, App
51	12	57.1	4	6	US-10-684-796-512	Sequence 512, App
52	12	57.1	4	6	US-10-684-796-546	Sequence 546, App
53	12	57.1	4	6	US-10-857-484-74	Sequence 74, Appl
54	12	57.1	4	7	US-11-030-232-341	Sequence 341, App
55	12	57.1	4	7	US-11-030-232-342	Sequence 342, App
56	12	57.1	4	7	US-11-030-232-344	Sequence 344, App
57	12	57.1	4	7	US-11-030-232-345	Sequence 345, App
58	12	57.1	4	7	US-11-030-232-347	Sequence 347, App
59	12	57.1	4	7	US-11-030-232-348	Sequence 348, App
60	12	57.1	4	7	US-11-038-326-11	Sequence 11, Appl
61	12	57.1	4	7	US-11-038-326-13	Sequence 13, Appl
62	12	57.1	4	7	US-11-051-267-23	Sequence 23, Appl
63	12	57.1	4	7	US-11-065-669-25	Sequence 25, Appl
64	12	57.1	4	7	US-11-066-697-1539	Sequence 1539, Ap
65	12	57.1	4	7	US-11-066-697-1553	Sequence 1553, Ap
66	12	57.1	4	7	US-11-066-697-1558	Sequence 1558, Ap
67	12	57.1	4	7	US-11-066-697-1563	Sequence 1563, Ap
68	12	57.1	4	7	US-11-080-973-25	Sequence 25, Appl
69	12	57.1	4	7	US-11-129-741-3986	Sequence 3986, Ap
70	11	52.4	2	1	PCT-IL05-00211-451	Sequence 451, App
71	11	52.4	2	1	PCT-IL05-00211-1047	Sequence 1047, Ap
72	11	52.4	2	1	PCT-IL05-00211-1365	Sequence 1365, Ap
73	11	52.4	2	1	PCT-IL05-00211-1526	Sequence 1526, Ap
74	11	52.4	2	1	PCT-IL05-00211-1537	Sequence 1537, Ap
75	11	52.4	3	1	PCT-IL05-00211-484	Sequence 484, App
76	11	52.4	3	1	PCT-IL05-00211-485	Sequence 485, App
77	11	52.4	3	1	PCT-IL05-00211-1071	Sequence 1071, Ap
78	11	52.4	3	1	PCT-IL05-00211-1072	Sequence 1072, Ap
79	11	52.4	3	1	PCT-IL05-00211-1382	Sequence 1382, Ap
80	11	52.4	3	1	PCT-IL05-00211-1383	Sequence 1383, Ap
81	11	52.4	3	1	PCT-IL05-00211-1588	Sequence 1588, Ap
82	11	52.4	3	1	PCT-IL05-00211-1589	Sequence 1589, Ap
83	11	52.4	3	1	PCT-IL05-00211-1599	Sequence 1599, Ap
84	11	52.4	3	1	PCT-IL05-00211-1600	Sequence 1600, Ap
85	11	52.4	4	1	PCT-US05-08075-26	Sequence 26, Appl
86	11	52.4	4	1	PCT-IL05-00211-516	Sequence 516, App
87	11	52.4	4	1	PCT-IL05-00211-517	Sequence 517, App
88	11	52.4	4	1	PCT-IL05-00211-518	Sequence 518, App
89	11	52.4	4	1	PCT-IL05-00211-1094	Sequence 1094, Ap
90	11	52.4	4	1	PCT-IL05-00211-1095	Sequence 1095, Ap
91	11	52.4	4	1	PCT-IL05-00211-1096	Sequence 1096, Ap
92	11	52.4	4	1	PCT-IL05-00211-1398	Sequence 1398, Ap
93	11	52.4	4	1	PCT-IL05-00211-1399	Sequence 1399, Ap
94	11	52.4	4	1	PCT-IL05-00211-1400	Sequence 1400, Ap
95	11	52.4	4	1	PCT-IL05-00211-1649	Sequence 1649, Ap
96	11	52.4	4	1	PCT-IL05-00211-1650	Sequence 1650, Ap
97	11	52.4	4	1	PCT-IL05-00211-1651	Sequence 1651, Ap
98	11	52.4	4	1	PCT-IL05-00211-1660	Sequence 1660, Ap

Sequence 1661, Ap
Sequence 1662, Ap

99 11 52.4 4 1 PCT-IL05-00211-1661
100 11 52.4 4 1 PCT-IL05-00211-1662

ALIGNMENTS

RESULT 1
US-10-892-402-108
; Sequence 108, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winessinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-108

Query Match 95.2%; Score 20; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
|:|
Db 1 RVPR 4

RESULT 2
US-10-892-402-144
; Sequence 144, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winessinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 144
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-144

Query Match 81.0%; Score 17; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1PR 4

Db 1 R1PR 4
|:|

RESULT 3
US-10-892-402-120
; Sequence 120, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winessinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 120
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-120

Query Match 76.2%; Score 16; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 R1PR 4
|:|
Db 1 R1PR 4

RESULT 4
US-10-529-163-28
; Sequence 28, Application US/10529163
; GENERAL INFORMATION:
; APPLICANT: YOUSEF, et al.
; TITLE OF INVENTION: Methods for Detecting Endocrine Cancer
; FILE REFERENCE: 11757.82USMO
; CURRENT APPLICATION NUMBER: US/10/529,163
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/414,107
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 28
; LENGTH: 3
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Peptide fragment of a Fluorogenic Synthetic Peptide
US-10-529-163-28

Query Match 71.4%; Score 15; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
|:|
Db 1 VPR 3

RESULT 5
US-10-529-163-30

; Sequence 30, Application US/10529163
; GENERAL INFORMATION: Yousef, et al.
; APPLICANT: YOUSEF, et al.
; TITLE OF INVENTION: Methods for Detecting Endocrine Cancer
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/529,163
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US 60/414,107
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide Portion of Trypsin Substrate
US-10-529-163-30

Query Match 71.4%; Score 15; DB 6; Length 3;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
: ||
DB 1 VPR 3

RESULT 6
US-10-892-402-11
; Sequence 11, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-11

Query Match 71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
: ||
DB 2 VPR 4

RESULT 7
US-10-892-402-59
; Sequence 59, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas

; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-59

Query Match 71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
: ||
DB 2 VPR 4

RESULT 8
US-10-892-402-100
; Sequence 100, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-100

Query Match 71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
: ||
DB 1 RVP 3

RESULT 9
US-10-892-402-104
; Sequence 104, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-104

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; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 104
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-104

Query Match          71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RIP 3
      |||
Db      1 RVP 3

RESULT 10
US-10-123-036B-17
; Sequence 17, Application US/10123036B
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF HEPATIC DISORDERS
; FILE REFERENCE: 0010872/0483963
; CURRENT APPLICATION NUMBER: US/10/123,036B
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: US 60/283,788
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-123-036B-17

Query Match          71.4%; Score 15; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IPR 4
      |||
Db      2 VPR 4

RESULT 11
US-11-106-715-87
; Sequence 87, Application US/11106715
; GENERAL INFORMATION:
; APPLICANT: Byrd, Devon
; APPLICANT: Youg, Alice
; APPLICANT: Hartley, James
; TITLE OF INVENTION: Compositions and Methods for Molecular Biology
; FILE REFERENCE: 0942.5230004
; CURRENT APPLICATION NUMBER: US/11/106,715
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US/10/633,690
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: US 60/400,704
; PRIOR FILING DATE: 2002-08-05
; PRIOR APPLICATION NUMBER: US 60/403,095
; PRIOR FILING DATE: 2002-08-14
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: thrombin cleavage site
US-11-106-715-87

Query Match          71.4%; Score 15; DB 7; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IPR 4
      |||
Db      2 VPR 4

RESULT 12
US-10-892-402-76
; Sequence 76, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-76

Query Match          66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 IPR 4
      |||
Db      1 LPR 3

RESULT 13
US-10-892-402-80
; Sequence 80, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-80

Query Match 66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
: ||
Db 1 LPR 3

RESULT 14

US-10-892-402-84
; Sequence 84, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-84

Query Match 66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 66.7%; Pred. No. 5.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPR 4
: ||
Db 1 LPR 3

RESULT 15

US-10-892-402-132
; Sequence 132, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; FILE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 132
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-132

Query Match 66.7%; Score 14; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RPR 4
: ||
Db 1 RPR 4

Search completed: June 20, 2005, 16:48:01
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:01:11 ; Search time 23 Seconds
(without alignments)
16.733 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 79:.*
1: Pirl:.*
2: Pirl:.*
3: Pirl:.*
4: Pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	11	57.9	4	2 I40870	phospholipase C (E
2	8	42.1	4	2 I40804	endoglucanase F -
3	6	31.6	3	3 PQ0010	angiotensin-conver
4	6	31.6	3	3 S13894	histidinol dehydro
5	6	31.6	4	2 T46827	hypothetical prote
6	6	31.6	4	2 PT0721	T-cell receptor be
7	5	26.3	3	3 A22565	R-phycoerythrin al
8	5	26.3	3	3 E37196	bradykinin-potenti
9	5	26.3	3	3 F37196	growth-modulating
10	5	26.3	3	3 GKHU	bursin - chicken
11	5	26.3	3	3 A60898	antho-RFamide neur
12	5	26.3	4	1 ECXAA	phagocytosis-stimu
13	5	26.3	4	2 A02147	hypothetical prote
14	5	26.3	4	2 D41654	hypothetical prote
15	5	26.3	4	2 I40505	hypothetical prote
16	5	26.3	4	2 A25844	antho-RF amide neu
17	5	26.3	4	2 S39390	myosin-light-chain
18	5	26.3	4	2 I61883	protamine p1 - ora
19	5	26.3	4	2 E44823	synaptosomal-assoc
20	5	26.3	4	2 S47552	ubiquitin - rat
21	5	26.3	4	2 I37013	protamine p1 - Cer
22	5	26.3	4	2 I84439	protamine p1 - sav
23	5	26.3	4	2 PL0146	carbon-monoxide de
24	5	26.3	4	2 FQ1273	neuropeptide Antho
25	5	26.3	4	2 A35779	neuropeptide Antho
26	5	26.3	4	2 A60418	FWRFamide - polych
27	5	26.3	4	2 PT0534	T-cell receptor be
28	5	26.3	4	2 ECNK	cardioexcitatory n
29	4	21.1	4	2 A37832	phenol 2-monooxyge

ALIGNMENTS

RESULT 1

I40870

phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)

C,Species: Clostridium perfringens

C,Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000

C,Accession: I40870

R;Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.

Microbiol. Immunol. 36, 603-613, 1992

A;Title: Role of the upstream region containing an intrinsic DNA curvature in the negativ

A;Reference number: I40870; MUID:92396045; PMID:1522810

A;Accession: I40870

22K superhelical D
cell surface adhes
glucan 1,4-alpha-g
hypothetical prote
schwannomin - mous
branched-chain-ami
globulin IV alpha
ribosomal protein
D-mannosate hydrol
Ig heavy chain CRD
T-cell receptor be
T-cell receptor be
T-cell receptor be
gamma subunit of P
COI intron 16 prot
thyloliberin - she
thyloliberin - Bom
TRH-like tripeptid
gene p20K protein
T-cell receptor be
tyrosine protein k
cytochrome-c oxida
thyloliberin - pig
spinal cord peptid
spinal cord peptid
thyrotropin-releas
thyroglobulin - do
protein D - Escher
hypothetical prote
metallothionein-A
Ig heavy chain CRD
T-cell receptor be
protein-glutamine
pallidipin - assas
carbon-monoxide de
T-cell receptor be
T-cell receptor be
tyrosine-melanocyt
T-cell receptor be
T-cell receptor be
T-cell receptor be
blood cell protein
starvation-induced
RPCH-related neuro
Ig mu chain V regi
T-cell receptor be
biotin A - Citroba
achatin-I - giant
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be

30 4 21.1 4 2 A61300
31 4 21.1 4 2 B43848
32 4 21.1 4 2 A27897
33 4 21.1 4 2 T30569
34 4 21.1 4 2 I54357
35 4 21.1 4 2 A40135
36 4 21.1 4 2 S09478
37 4 21.1 4 2 S17255
38 3 15.8 4 2 I57745
39 3 15.8 4 2 PT0271
40 3 15.8 4 2 PT0633
41 3 15.8 4 2 PT0551
42 3 15.8 4 2 PT0697
43 2 10.5 4 2 A48360
44 2 10.5 4 2 I38888
45 1 5.3 3 3 RSHST
46 1 5.3 3 3 A92971
47 1 5.3 3 3 RHTDIO
48 1 5.3 3 3 A43391
49 1 5.3 3 3 I50412
50 1 5.3 3 3 PT0578
51 1 5.3 3 3 I78890
52 1 5.3 3 3 T13892
53 1 5.3 3 3 RHPGT
54 1 5.3 3 3 A23751
55 1 5.3 3 3 B23751
56 1 5.3 3 3 A33802
57 1 5.3 4 2 S18401
58 1 5.3 4 2 A41890
59 1 5.3 4 2 S43014
60 1 5.3 4 2 I51049
61 1 5.3 4 2 PT0240
62 1 5.3 4 2 A53284
63 1 5.3 4 2 A26209
64 1 5.3 4 2 S55238
65 1 5.3 4 2 PL0140
66 1 5.3 4 2 PT0645
67 1 5.3 4 2 PT0677
68 1 5.3 4 2 A32039
69 0 0.0 3 3 PT0636
70 0 0.0 3 3 PT0571
71 0 0.0 3 3 PT0622
72 0 0.0 3 3 S68328
73 0 0.0 4 2 S53508
74 0 0.0 4 2 A34626
75 0 0.0 4 2 A43959
76 0 0.0 4 2 B53284
77 0 0.0 4 2 I40697
78 0 0.0 4 2 A32480
79 0 0.0 4 2 PT0696
80 0 0.0 4 2 PT0711
81 0 0.0 4 2 PT0661
82 0 0.0 4 2 PT0712
83 0 0.0 4 2 PT0698
84 0 0.0 4 2 PT0706
85 0 0.0 4 2 PT0675
86 0 0.0 4 2 PT0566

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417
C:Genetics:
A:Gene: plc
C:Keywords: phosphoric diester hydrolase

Query Match 57.9%; Score 11; DB 2; Length 4;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKR 4
:||
Db 1 MKR 3

RESULT 2
I40804
endoglucanase F - Clostridium thermocellum (fragment)
C:Species: Clostridium thermocellum
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I40804
R:Mishra, S.; Beguin, P.; Aubert, J.
J. Bacteriol. 173, 80-85, 1991

A>Title: Transcription of clostridium thermocellum endoglucanase genes celf and celd.
A:Reference number: I40804; MUID:91100322; PMID:1987137
A:Accession: I40804
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <RES>
A:Cross-references: UNIPROT:P26224; GB:M64363; NID:g144771
C:Genetics:
A:Gene: celf
A:Start codon: TTG

Query Match 42.1%; Score 8; DB 2; Length 4;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VKR 4
:||
Db 1 MKK 3

RESULT 3
PQ0010
angiotensin-converting enzyme inhibitor (FLP-3) - common fig
N:Alternate names: ficus latex peptide 3
C:Species: Ficus carica (common fig)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: PQ0010
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
Agric. Biol. Chem. 53, 2763-2767, 1989
A>Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
A:Reference number: PQ0008
A:Accession: PQ0010
A:Molecule type: protein
A:Residues: 1-3 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 31.6%; Score 6; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
:||
Db 2 VR 3

RESULT 4
S13894

histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C:Species: Brassica oleracea (wild cabbage)
C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: S13894
R:Nagai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A>Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A:Reference number: S13894; MUID:91112783; PMID:1989490
A:Accession: S13894
A:Molecule type: protein
A:Residues: 1-3 <NAG>
A:Experimental source: var. capitata
C:Keywords: dimer; NAD; oxidoreductase

Query Match 31.6%; Score 6; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
:||
Db 2 MK 3

RESULT 5
T46627
hypothetical protein c4 - loblolly pine
C:Species: Pinus taeda (loblolly pine)
C>Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: T46627
R:Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A>Description: Cloning of a chitinase homolog which lacks chitin binding sites and is do
A:Reference number: Z23105
A:Accession: T46627
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4 <CHA>
A:Cross-references: EMBL:U31309; NID:g974285; PID:g974292
A:Experimental source: strain s6PT2xs6PT3; 8 month seedlings

Query Match 31.6%; Score 6; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
:||
Db 1 MK 2

RESULT 6
PT0721
T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: PT0721
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0721
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-4 <FEE>
A:Cross-references: UNIPROT:Q8JZN5; UNIPROT:P54729; UNIPROT:Q8CBY1; UNIPROT:Q8COCO
A:Experimental source: newborn thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 31.6%; Score 6; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RV 2
|:

Db 2 RL 3

RESULT 7

A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C:Species: Gastroclonium coulteri
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: A22565
R:Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
A:Reference number: A22565; MUID:85182601; PMID:3886644
A:Accession: A22565
A:Molecule type: protein
A:Residues: 1-3 <KLO>

Query Match 26.3%; Score 5; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0;

Query 1 R 1 DB 3; Length 3;

Db 3 R 3

RESULT 8

E37196
bradykinin-potentiating peptide 5 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C:Accession: E37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: E37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
A:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0;

Query 3 K 3 DB 3; Length 3;

Db 3 K 3

RESULT 9

F37196
bradykinin-potentiating peptide 6 - island jararaca
C:Species: Bothrops insularis (island jararaca)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: F37196
R:Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: F37196
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-3 <CIN>
A:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0;

Query 3 K 3 DB 3; Length 3;

Db 3 K 3

QY 3 K 3

Db 2 K 2

RESULT 10

GKHU
growth-modulating peptide - human
C:Species: Homo sapiens (man)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: A01421
R:Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A:Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A:Reference number: A01421; MUID:77162369; PMID:858356
A:Accession: A01421
A:Molecule type: protein
A:Residues: 1-3 <SCH>
A:Note: this serum tripeptide is found to stimulate growth of some cell types and to inhibit

Query Match 26.3%; Score 5; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0;

Query 3 K 3 DB 3; Length 3;

Db 3 K 3

RESULT 11

A60898
bursin - chicken
C:Species: Gallus gallus (chicken)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C:Accession: A60898
R:Audhya, T.; Koon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 231, 997-999, 1986
A:Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the
A:Reference number: A60898; MUID:86122916; PMID:3484838
A:Accession: A60898
A:Molecule type: protein
A:Residues: 1-3 <AUD>
A:Keywords: amidated carboxyl end; hormone
F:3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 26.3%; Score 5; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 1; Conservative 0;

Query 3 K 3 DB 3; Length 3;

Db 1 K 1

RESULT 12

ECXAA
antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)
C:Species: Anthopleura elegantissima
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A26666
R:Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A:Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemone
A:Reference number: A26666; MUID:87092339; PMID:2879288
A:Accession: A26666
A:Molecule type: protein
A:Residues: 1-4 <GRI>
A:Cross-references: UNIPROT:P10419
A:Comment: The function of this peptide is not known but it could act as a transmitter at
C:Comment: Synthetic and natural peptides had identical properties.
C:Superfamily: RFamide neuropeptide
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:/4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
DB 3 R 3

RESULT 13

A02147
phagocytosis-stimulating peptide (tuftsin) - human
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02147
R:Nishioaka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A:Title: The characteristics, isolation and synthesis of the phagocytosis stimulating peptide
A:Reference number: A02147; PMID:72187087; PMID:4112769
A:Accession: A02147
A:Molecule type: protein
A:Residues: 1-4 <NIS>
A:Cross-references: UNIPROT:P01858
A:Note: a peptide having the same structure, physical properties, and biological activity
R:Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3386-3392, 1967
A:Reference number: A37502; PMID:68091045; PMID:4169272
A:Contents: annotation; immunoglobulin class
C:Comment: An IGG (called leucokinin) binds reversibly to the cell membrane of neutrophils
n is essential for maximum stimulation of the phagocytic activity of neutrophils.
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 26.3%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
DB 2 K 2

RESULT 14

D41654
hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
C:Species: Haemophilus parainfluenzae
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 24-Feb-1995
C:Accession: D41654
R:Kroll, J.S.; Langford, P.R.; Loynds, B.M.
J. Bacteriol. 173, 7449-7457, 1991
A:Title: Copper-zinc superoxide dismutase of Haemophilus influenzae and Haemophilus parainfluenzae
A:Reference number: A41654; PMID:92041655; PMID:1938942
A:Accession: D41654
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <KRO>

Query Match 26.3%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
DB 2 R 2

RESULT 15

I40505
hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
C:Species: Bacillus stearothermophilus
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40505

R:Waye, M.M.; Winter, G.
Eur. J. Biochem. 158, 505-510, 1986
A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene
A:Reference number: I40503; PMID:86274732; PMID:3525162
A:Accession: I40505
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-4 <RES>
A:Cross-references: EMBL:X04193; NID:940233; PIDN:CAA27783.1; PID:G580944

Query Match 26.3%; Score 5; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
DB 4 K 4

Search completed: June 20, 2005, 16:34:36
Job time : 24 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 15:59:16 ; Search time 109.5 Seconds
(without alignments)
18.706 Million cell updates/sec

Title: US-09-885-914B-3
Perfect score: 19
Sequence: 1 RVKR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	42.1	3	1 LUXE VIBFI	P24272 vibrio fisc
2	8	42.1	4	1 FYRI ANTEL	P58706 anthopleura
3	6	31.6	4	2 Q08433	Q08433 rattus sp.
4	5	26.3	3	1 GRWM HUMAN	P01157 homo sapien
5	5	26.3	4	1 DCMS PSECH	P19918 pseudomonas
6	5	26.3	4	1 FAR3_HIRME	P42562 hirudo medi
7	5	26.3	4	1 FAR4_HIRME	P42563 hirudo medi
8	5	26.3	4	1 FLRF_HIRME	P58705 anthopleura
9	5	26.3	4	1 FLRN_HIRME	P42561 hirudo medi
10	5	26.3	4	1 FLRN ANTEL	P58707 anthopleura
11	5	26.3	4	1 FMRF_MACNI	P01162 macrocallis
12	5	26.3	4	1 TUFT_HUMAN	P01858 homo sapien
13	5	26.3	4	2 Q96AT0	Q96AT0 homo sapien
14	4	21.1	4	1 EOSI HUMAN	P02731 homo sapien
15	4	21.1	4	1 YLME YEAST	P36515 saccharomyc
16	3	15.8	4	1 ILMI SEPOF	P83568 sephia offic
17	1	5.3	3	1 THYL_BOMOR	P62970 bomina ori
18	1	5.3	3	1 THYL_NOTVI	P62971 notophthalm
19	1	5.3	3	1 THYL_PIG	P62968 sus scrofa
20	1	5.3	3	1 THYL_SHEEP	P62969 ovis aries
21	1	5.3	4	1 DCML_PSECH	P19916 pseudomonas
22	0	0.0	2	1 GWA_SEPOF	P83570 sephia offic
23	0	0.0	4	1 ACHI_ACHFU	P35904 achatina fu
24	0	0.0	4	1 OCPI_OCTMI	P58648 octopus min
25	0	0.0	4	1 OCP3_OCTMI	P58649 octopus min
26	0	0.0	4	2 Q16047	Q16047 homo sapien

ALIGNMENTS

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RESULT 1
LUXE_VIBFI
ID LUXE_VIBFI STANDARD; PRT; 3 AA.
AC P24272;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acyl-
DE protein synthetase) (Fragment).
GN Name=luxE;
OS Vibrio fischeri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=668;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91072226; PubMed=2254256;
RA Swartzman E., Kapoor S., Graham A.P., Meighen E.A.;
RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
RT site for the lux operon.";
RL J. Bacteriol. 172:6797-6802(1990).
CC -!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
CC is a component of the fatty acid reductase complex responsible for
CC converting tetradecanoic acid to the aldehyde which serves as
CC substrate in the luciferase-catalyzed reaction.
CC -!- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
CC an acyl-protein thioester.
CC -!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
CC -!- SIMILARITY: Belongs to the luxE family.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL; M62812; -; NOT ANNOTATED_CDS.
DK Ligase; Luminescence.
FT NON_TER 1
SQ SEQUENCE 3 AA; 374 MW; 5AA3303000000000 CRC64;

Query Match 42.1%; Score 8; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VK 3
Db 1 IK 2

RESULT 2
FYRI_ANTEL
ID FYRI_ANTEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;
RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
RT biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its des-
RT phenyllactyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).

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RN FUNCTION.
RP MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Riamide and Antho-Riamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron specific.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT CHAIN 1 4 Antho-Riamide I.
FT CHAIN 2 4 Antho-Riamide II.
FT MOD_RES 1 1 3-phenyllactic acid.
FT MOD_RES 4 4 Isoleucine amide.
SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 42.1%; Score 8; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RV 2
Db 3 RI 4

RESULT 3
Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bilirubin UDP-glucuronosyltransferase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Gunn;
RX MEDLINE=91282758; PubMed=1840486;
RA Sato H., Aono S., Kashiwamata S., Koiwai O.;
RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
RT hyperbilirubinemic Gunn rat.";
RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).
DR EMBL; S38636; AAB19259.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Transferase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match 31.6%; Score 6; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VK 3
Db 3 LK 4

RESULT 4
GRWM HUMAN
ID GRWM HUMAN STANDARD; PRT; 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
RL Experimentia 33:324-325(1977).
CC -!- MISCELLANEOUS: This serum tripeptide has been found to stimulate
CC growth of some cell types and to inhibit other types in vitro.
CC GO; GO:0001558; P:regulation of cell growth; NAS.
DR Direct protein sequencing.
KW SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
Db 3 K 3

RESULT 5
DCMS_PSECH STANDARD; PRT; 4 AA.
ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19518;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit S) (CO-DH S) (Fragment).
GN Name=cutS;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -!- COFACTOR: Binds 2 2Fe-2S clusters (By similarity).
CC -!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
CC subunit.
DR PIR; PL0146; PL0146.
KW 2Fe-2S; Direct protein sequencing; Iron; Iron-sulfur; Metal-binding;
KW Oxidoreductase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F0000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 K 3
Db 3 K 3

RESULT 6
FAR3_HIRME STANDARD; PRT; 4 AA.
ID FAR3_HIRME STANDARD; PRT; 4 AA.
AC P42562;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide YLRP-amide.

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OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 CC Amidation; Direct protein sequencing; Neuropeptide.
 KW MOD_RES 4 4 Phenylalanine amide.
 FT MOD_RES 4 AA; 598 MW; 69D4073B30000000 CRC64;
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 Db 3 R 3
 RESULT 7
 ID_FARP4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995. (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide YMRP-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 CC Amidation; Direct protein sequencing; Neuropeptide.
 KW MOD_RES 4 4 Phenylalanine amide.
 FT MOD_RES 4 AA; 616 MW; 69D4068B30000000 CRC64;
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 Db 3 R 3
 RESULT 8
 ID_FFKA_ATEL STANDARD; PRT; 4 AA.
 AC P58705;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antho-KAamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaeae; Actinidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=92028852; PubMed=1681803;
 RA Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
 RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), a novel neuropeptide from sea anemones.";
 RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
 RN [2]
 RP FUNCTION.
 RX MEDLINE=93391436; PubMed=8397415;
 RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
 RT "The expansion behaviour of sea anemones may be coordinated by two inhibitory neuropeptides, Antho-KAamide and Antho-RKamide.";
 RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron specific.
 DR PIR; JQ1273; JQ1273.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 1 1 3-phenyllactic acid.
 FT MOD_RES 4 4 Alanine amide.
 SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 K 3
 Db 3 K 3
 RESULT 9
 ID_FLRF_HIRME STANDARD; PRT; 4 AA.
 AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FLRFamide.
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=H.medicalinalis;
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908(1991).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=H.trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma trivolvis.";
 RL Peptides 15:31-36(1994).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A000000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1

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Db          3 R 3

RESULT 10
FLRN ANTEL          STANDARD;          PRT;          4 AA.
AC P58707;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Antho-RNamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=90319122; PubMed=1973541;
RA Grimelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA Reinecheid R.K., Nothacker H.-P., Staley A.L.;
RT "Isolation of D-3-phenylacetyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT anemone neuropeptide containing an unusual amino-terminal blocking
RT group."
RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Neuron specific.
CC -|- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
DR PIR; A35779; A35779.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 1 1 3-phenylacetic acid.
FT MOD_RES 4 4 Asparagine amide.
SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

RESULT 11
PMRF_MACNI
ID PMRF_MACNI          STANDARD;          PRT;          4 AA.
AC P01162;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE PMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocaltista nimboza (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
OC Veneroidea; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC SPECIES=M.nimboza; TISSUE=Cerebral pedal, and Visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide."
RL Science 197:670-671 (1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RC SPECIES=M.nimboza; TISSUE=Ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
RT from the central ganglia of a bivalve mollusc."
RL Prep. Biochem. 7:261-281 (1977).

RN [3]
SEQUENCE.
RC SPECIES=N.virens; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;
RX MEDLINE=90259866; Price D.A.;
RA Krajniak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens."
RL Peptides 11:75-77 (1990).
RN [4]
SEQUENCE.
RC SPECIES=H.medicinalis;
RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of RFamide neuropeptides in the medicinal leech."
RL Peptides 12:897-908 (1991).
RN [5]
SEQUENCE.
RC SPECIES=H.trivolvis; TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis."
RL Peptides 15:31-36 (1994).
CC -|- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
CC activities include augmentation, induction, and regularization of
CC cardiac contraction.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the FARP (PMRFamide related peptide)
CC family.
DR PIR; A01426; ECNK.
DR PIR; A60418; A60418.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 4 4 Phenylalanine amide.
SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;

Query Match 26.3%; Score 5; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R 1
Db 3 R 3

RESULT 12
TUFT_HUMAN
ID TUFT_HUMAN          STANDARD;          PRT;          4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
RT stimulating peptide tuftsin."
RL Biochem. Biophys. Res. Commun. 47:172-179 (1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic
RT activity of human polymorphonuclear leucocyte."
RL Biochemistry 6:3386-3392 (1967).
CC -|- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the
CC cell membrane of neutrophils in the blood. Leucokininase on the
CC membrane releases the active peptide tuftsin from the gamma chain.

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CC Tuftsin is essential for maximum stimulation of the phagocytic
 CC activity of neutrophils.
 DR PIR; A02147; A02147.
 DR MIM; 191150; -.
 DR GO; 0003823; F:antigen binding; NAS.
 DR GO; 0006909; P:phagocytosis; NAS.
 DR KW Direct protein sequencing.
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;
 Query Match 26.3%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 K 3
 Db 2 K 2
 RESULT 13
 Q96AT0 PRELIMINARY; PRT; 4 AA.
 ID Q96AT0
 AC Q96AT0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE FLJ30656 protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR ENBL; BC016791; AAH16791.2; -.
 SQ SEQUENCE 4 AA; 512 MW; 633DCB58F0000000 CRC64;
 Query Match 26.3%; Score 5; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 K 3
 Db 4 K 4
 RESULT 14
 E0SI_HUMAN
 ID E0SI_HUMAN STANDARD; PRT; 4 AA.
 AC P02731;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Eosinophilic tetrapeptides.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=76078412; PubMed=1060093;
 RA Goetzl E.J., Austen K.F.;
 RT "Purification and synthesis of eosinophilic tetrapeptides of
 RT human lung tissue: identification as eosinophil chemotactic factor of
 RT anaphylaxis";
 RL Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).
 CC -I- MISCELLANEOUS: These peptides are released from mast cells in lung
 CC (and other tissues) during hypersensitivity reactions
 CC (anaphylaxis). Their activities, preferentially affecting
 CC eosinophils, include chemotaxis, chemotactic deactivation, release
 CC of enzymes, and stimulation of the hexose monophosphate shunt.
 CC GO: 0006935; P:chemotaxis; IDA.
 DR GO: 0006955; P:immune response; IDA.
 KW Direct protein sequencing.
 FT VARIANT 1
 FT 1 V -> A (in other peptide).
 SQ SEQUENCE 4 AA; 390 MW; 6B05B862A0000000 CRC64;
 Query Match 21.1%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 V 2
 Db 1 V 1
 RESULT 15
 YLMI_YEAST
 ID YLMI_YEAST STANDARD; PRT; 4 AA.
 AC P36515;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
 GN Names=Yml1;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
 RA Grohmann L., Graack H.-R., Kruff V., Choi T., Goldschmidt-Reisin S.,
 RA Kitakawa M.;
 RT "Extended N-terminal sequencing of proteins of the large ribosomal
 RT subunit from yeast mitochondria";
 RL FEBS Lett. 284:51-56(1991).
 CC -I- FUNCTION: Putative component of the large subunit of mitochondrial
 CC ribosome.
 CC -I- SUBCELLULAR LOCATION: Mitochondrial.
 DR PIR; S17255; S17255.
 KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
 FT NON_TER 4
 SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
 Query Match 21.1%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 V 2

Db 2 V 2

Search completed: June 20, 2005, 16:33:43
Job time : 109.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 14:16:51 ; Search time 113.5 Seconds
(without alignments)
13.630 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 19815

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	4	6	Aae35573 Furin cle
2	19	100.0	4	8	Adj57391 Furin inh
3	16	84.2	4	2	Ray30777 Peptide u
4	16	84.2	4	3	Ray84215 Amino aci
5	16	84.2	4	4	Aab97408 Site-1 pr
6	16	84.2	4	4	Aab97427 Site-1 pr
7	16	84.2	4	5	Aae24432 Transport
8	16	84.2	4	5	Aao14861 Furin sub
9	16	84.2	4	6	Abp71148 Human pro
10	16	84.2	4	6	Ada10587 Eglin c v
11	16	84.2	4	7	Add84924 Tetrapept
12	16	84.2	4	8	Adg19004 Multimeri
13	16	84.2	4	8	Adj57390 Peptide f
14	15	78.9	4	2	Aar37629 Sequence
15	15	78.9	4	2	Aar60593 proins.RT
16	15	78.9	4	5	Aau75632 Human myo
17	15	78.9	4	5	Aau78849 Human ins
18	15	78.9	4	5	Aae18671 Zebra fis
19	15	78.9	4	5	Aao17049 Furin sit
20	15	78.9	4	6	Abg73570 Human pro
21	15	78.9	4	6	Aao30152 Spectrozy
22	15	78.9	4	6	Aae29827 Spectrozy
23	15	78.9	4	6	Aae29796 Spectrozy
24	15	78.9	4	6	Ada10588 Eglin c v
25	15	78.9	4	6	Adb17421 Human ins

26	15	78.9	4	7	ABU10024	Abu10024 Alpha-MSH
27	15	78.9	4	7	ADB97569	ADB97569 Protease
28	15	78.9	4	8	ADI28884	ADI28884 Human ser
29	15	78.9	4	8	ADJ57392	Adj57392 Furin inh
30	14	73.7	4	1	AAP20059	Enzyme su
31	14	73.7	4	2	AAR37635	Sequence
32	14	73.7	4	2	AAR85940	Peptidase
33	14	73.7	4	3	AAy44372	Tetrahase
34	14	73.7	4	4	AAU07641	Amino aci
35	14	73.7	4	4	AAU07641	Wild-type
36	14	73.7	4	4	AAU07641	Wild-type
37	14	73.7	4	5	AAU07641	Wild-type
38	14	73.7	4	5	AAU07641	Wild-type
39	14	73.7	4	5	AAU07641	Wild-type
40	14	73.7	4	5	AAU07641	Wild-type
41	14	73.7	4	6	ABP98103	Amino aci
42	14	73.7	4	6	ABR40173	Marburg v
43	14	73.7	4	7	ADH10700	Streptomy
44	14	73.7	4	8	ADQ80880	Subtilisi
45	13	68.4	4	2	AAR37630	Sequence
46	13	68.4	4	2	AAR48281	Nuclea r
47	13	68.4	4	2	AAR60559	Tissue pl
48	13	68.4	4	2	AAR60594	proins.RQ
49	13	68.4	4	2	AAR51491	Human A-m
50	13	68.4	4	2	AAR52965	Human A-m
51	13	68.4	4	2	AAR64811	ScFv-Lys
52	13	68.4	4	2	AAR65180	Dibasic a
53	13	68.4	4	2	AAW71193	Peptide u
54	13	68.4	4	2	AAW70904	Amino aci
55	13	68.4	4	2	AAW44279	Human thy
56	13	68.4	4	2	AAW96353	Nucleus 1
57	13	68.4	4	3	AAy57104	Linker am
58	13	68.4	4	3	AAy82083	HIV 168P
59	13	68.4	4	3	AAy82085	HIV enhan
60	13	68.4	4	3	AB14217	HIV SF162
61	13	68.4	4	4	AAE00920	Cleavage
62	13	68.4	4	4	AAE72635	Mammalian
63	13	68.4	4	4	AAE72639	Mammalian
64	13	68.4	4	4	AAE62231	PA protei
65	13	68.4	4	5	AAE14288	Thymosin
66	13	68.4	4	5	AAU78847	Human ins
67	13	68.4	4	5	ABP77181	Human mat
68	13	68.4	4	5	AAE24419	Transport
69	13	68.4	4	5	ABG31270	Human fac
70	13	68.4	4	5	AAO17055	Peptide a
71	13	68.4	4	5	ABO9213	HIV Env c
72	13	68.4	4	5	AAW52115	Anthrax P
73	13	68.4	4	5	ABG73639	PRPV type
74	13	68.4	4	5	ABG92988	Nucleus 1
75	13	68.4	4	6	ABR57047	Furin-rec
76	13	68.4	4	6	ABP98107	Amino aci
77	13	68.4	4	6	ABU08964	ADAM meta
78	13	68.4	4	6	ABP56583	Endoplasm
79	13	68.4	4	6	ABP71147	Human pro
80	13	68.4	4	6	ADB17417	Human ins
81	13	68.4	4	7	ADB87742	HIV-1 str
82	13	68.4	4	7	ADC13968	Rheumatol
83	13	68.4	4	7	ADC73270	Yeast Int
84	13	68.4	4	7	ADD66262	HIV-1 Env
85	13	68.4	4	8	ADF61758	Exemplary
86	13	68.4	4	8	ADG18991	Multimeri
87	13	68.4	4	8	ADI05537	Novel ade
88	13	68.4	4	8	ADJ57388	Peptide f
89	13	68.4	4	8	ADJ58925	Human pro
90	13	68.4	4	8	ADK42329	Antibacte
91	13	68.4	4	8	ADP44031	Human thy
92	13	68.4	4	8	ADQ30899	Newcastle
93	13	68.4	4	8	ADS82099	Cleavage
94	12	63.2	4	2	AAR37631	Sequence
95	12	63.2	4	2	AAR38742	KEX2 clea
96	12	63.2	4	2	AAR59927	Alpha 1-a
97	12	63.2	4	2	AAR60595	proins.KT
98	12	63.2	4	2	AAR90378	Synthetic

99 12 63.2 4 2 AAW25085 Aaw25085 Protein C
100 12 63.2 4 2 AAY20463 Aay20463 Human mic

ALIGNMENTS

RESULT 1
AAE35573 ID AAE35573 standard; peptide; 4 AA.

XX AC AAE35573;
XX AC
DT 17-JUN-2003 (first entry)
XX
DE Furin cleavable linker peptide.
XX
XX Fusion agent; immunogenic; proliferative disease; infectious disease;
KW cancer; therapy; vaccine; melanoma; Trojan antigen; TA.
XX
OS Unidentified.
XX
XX WO200294994-A2.
XX
XX 28-NOV-2002.
XX
XX 20-MAY-2002; 2002WO-US015992.
XX
XX 18-MAY-2001; 2001US-0291874P.
XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
XX Celis E;
XX
XX WPI; 2003-140367/13.
XX
XX Fusion agent useful for preventing and treating an infectious disease, or
PT a proliferative disease, such as cancer, comprises a transport domain,
PT two cleavage sites, a peptide epitope and a biologically active agent.
XX
XX Example 1; Page 37; 72pp; English.

XX The invention relates to a fusion agent (Trojan antigen; TA) comprising a
CC transport domain, two cleavage sites, a peptide epitope recognised by an
CC antigen-specific receptor on an effector T-lymphocyte precursor cell and
CC a biologically active agent, where there is a cleavage site between the
CC peptide epitope and the biologically active agent and between each
CC biologically active agent. The fusion agent is used to make a cell
CC immunogenic or antigenic. It is also useful for preventing and treating
CC an infectious disease such as viral, bacterial, protozoal, fungal or
CC yeast disease, or proliferative disease such as cancer (e.g. melanoma,
CC neural tissue, gastrointestinal, breast, lung, ovarian, testicular,
CC prostate, cervical, bladder, vaginal, liver, renal, bone, haematological
CC or vascular tissue cancer). The invention is used as vaccines. The
CC present sequence is furin cleavable linker peptide. This peptide is used
CC in the exemplification of the invention
XX

XX Sequence 4 AA;
Query Match 100.0%; Score 19; DB 6; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RVKR 4

RESULT 2
ADJ57391 ID ADJ57391 standard; peptide; 4 AA.
XX
XX AC ADJ57391;

XX 06-MAY-2004 (first entry)
DT
XX
DE Furin inhibitor peptide.
XX
XX Convertase; inhibitor; furin; antiinflammatory; vulnerary;
KW ophthalmological; dermatological; nephrotropic; hepatotropic; vasotropic;
KW antifertility; respiratory-gen.; cardiant; CNS-gen.; cerebroprotective;
KW neuroprotective; nootropic; cytostatic; antiarthritic;
KW antiarteriosclerotic.
XX
OS Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "dec-Arg"
FT Modified-site 4 /note= "Arg-cmk"
FT
XX WO2004009113-A1.
XX
XX 29-JAN-2004.
XX
XX 23-JUL-2003; 2003WO-GB003159.
XX
XX 24-JUL-2002; 2002GB-00017136.
XX (RENO-) RENOVO LTD.
XX
XX Ferguson MWJ, Brunner G;
PI WPI; 2004-180270/17.
XX
XX Use of a convertase inhibitor in the manufacture of a medicament for
PT reducing scarring during the healing of wounds or reducing fibrosis in
PT the treatment of fibrotic conditions.
XX
XX Example; Page 28; 43pp; English.

XX The present sequence is that of a furin inhibitor peptide. This was used
CC in an example from the invention which showed that furin-like enzymes are
CC involved in platelet-mediated latent transforming growth factor-beta (TGF
CC -beta) activation. The inventors have established that convertase enzymes
CC such as furin act, both extracellularly and intracellularly, to cause the
CC activation of latent transforming growth factor-beta (TGF-beta) in the
CC extracellular space at the site of a wound of a fibrotic conditions.
CC Thus, the present invention relates to use of convertase inhibitors for
CC the reduction of scarring during the healing of wounds, for reducing to
CC fibrosis in the treatment of fibrotic conditions, for treating wounds to
CC prevent scar formation, for preventing scarring of the eye, nervous
CC tissue or intestines, dermal scarring and scarring following a burn. The
CC fibrotic condition is a fibrotic disorder such as glomerulonephritis,
CC cirrhosis of the liver, fibrotic disease, adhesions and restenosis (all
CC claimed). The convertase inhibitor can also be used for the treatment of
CC hypertrophic and keloid scars, scarring in the heart, scarring of the gut,
CC scarring in the pelvis in the region of the fallopian tubes leading to
CC infertility, scarring following injury to the muscles, scarring or
CC fibrosis following injury to tendons and ligaments, which can result in
CC serious loss of function, liver fibrosis, pulmonary fibrosis,
CC scleroderma, myocardial hibernation, fibrosis following myocardial
CC infarction, central nervous system fibrosis following a stroke or
CC neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
CC vitreoretinopathy, arthritis, arteriosclerosis and cancer.

XX Sequence 4 AA;

Query Match 100.0%; Score 19; DB 8; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RVKR 4

RESULT 3
 AAY30777
 ID AAY30777 standard; peptide; 4 AA.
 XX
 AC AAY30777;
 XX
 DT 25-NOV-1999 (first entry)
 XX
 DE Peptide used to determine substrate specificity of an endo-type protease.
 XX
 KW Endo-type cysteine protease; cod fish milt; food; beverage.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "protected with -BOC"
 FT Modified-site 4 /note= "-MAC attached"
 FT JPL1225756-A.
 PN
 XX 24-AUG-1999.
 XX
 PF 10-FEB-1998; 98JP-00042973.
 XX
 PR 10-FEB-1998; 98JP-00042973.
 XX
 PA (HASE) HASEGAWA CO LTD.
 XX
 DR WPI; 1999-553905/47.
 XX
 PT New cysteine protease - useful in food/beverage products and pharmaceuticals.
 PT
 PS Disclosure; Page 4; 9pp; Japanese.
 XX
 CC The specification describes an endo-type cysteine protease that has substrate specificity and cleaves the C terminus side of the sequence of Lys-Arg and Arg-Arg. The enzyme has the molecular weight of 72,000 based on SDS-PAGE and an isoelectric point of 5.22. The endo-type cysteine protease is obtained from cod fish milt. The enzyme is used in food and beverage products and pharmaceuticals. The present sequence represents a peptide used to determine specificity of the enzyme
 XX
 SQ Sequence 4 AA;
 Query Match 84.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVKR 4
 ||:|
 Db 1 RVRK 4
 RESULT 4
 AAY84215
 ID AAY84215 standard; peptide; 4 AA.
 XX
 AC AAY84215;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Amino acid sequence of a peptide.
 XX
 KW Modulator; sterol-regulated Site-1 protease; cholesterol;
 KW sterol regulatory element binding protein; SREBP; lipid synthesis;
 KW fatty acid biosynthesis; site-1 protease; protease inhibitor;
 KW serum cholesterol; hypercholesterolemia; lipid metabolism.
 XX

OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Boc attached"
 FT Misc-difference 4 /note= "attached to MCA"
 FT
 XX
 PN W0200009677-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 13-AUG-1999; 99WO-US018544.
 XX
 PR 14-AUG-1998; 98US-0096571P.
 PR 23-JUL-1999; 99US-00360237.
 XX
 PA (TEXA) UNIV TEXAS SYSTEM.
 PA (BROW/) BROWN M S.
 PA (CHEN/) CHENG D.
 PA (ESPE/) ESPENSHADE P J.
 PA (GOLD/) GOLDSTEIN J L.
 PA (RAWS/) RAWSON R B.
 PA (SAXA/) SAKAI J.
 XX
 PI Brown MS, Cheng D, Espenshade PJ, Goldstein JL, Rawson RB;
 PI Sakai J;
 XX
 DR WPI; 2000-224327/19.
 XX
 PT Novel assay for identifying modulators of sterol-regulated Site-1 protease useful for the treatment of hypercholesterolemia, involves identifying an agent capable of down regulating Site-1 protease activity.
 PT
 XX Example 11; Page 106; 172pp; English.
 XX
 CC The specification describes a method for identifying modulators of a sterol-regulated Site-1 protease. Site-1 protease cleaves sterol regulatory element binding proteins (SREBPs) in the endoplasmic reticulum, initiating release from membranes and activating lipid synthesis. The modulators therefore also modulate cholesterol and fatty acid biosynthesis. The method comprises selecting an agent capable of down regulating Site-1 protease and formulating a composition comprising the agent. The site-1 protease inhibitors are useful for treating a patient for elevated serum cholesterol. Diseases treated include hypercholesterolemia and other lipid metabolism associated conditions.
 CC The present sequence was used in the course of the invention
 XX
 SQ Sequence 4 AA;
 Query Match 84.2%; Score 16; DB 3; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RVKR 4
 ||:|
 Db 1 RVRK 4
 RESULT 5
 AAB97408
 ID AAB97408 standard; peptide; 4 AA.
 XX
 AC AAB97408;
 XX
 DT 27-JUL-2001 (first entry)
 XX
 DE Site-1 protease inhibition method related peptide #2.
 XX
 KW Site-1 protease; S1P; sterol regulatory element binding protein; SREBP;
 KW fatty acid synthesis; cholesterol homeostasis; triglyceride.
 XX
 OS Synthetic.

```

XX Key Location/Qualifiers
FH Modified-site 1 /label= OTHER
FT
FT
FT Modified-site 4 /note= "modified by t-butyloxycarbonyl"
FT
FT Modified-site 4 /label= OTHER
FT
FT /note= "modified by 4-methyl-coumaryl-7-amide"
XX
XX WO200127138-A2.
XX
XX 19-APR-2001.
XX
XX 11-OCT-2000; 2000WO-US028428.
XX
XX 13-OCT-1999; 99US-0159236P.
XX
XX (TULA-) TULARIK INC.
XX (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
XX
XX Jaen JC, Li L, Brown MS, Goldstein JL, Cheng D;
XX WPI; 2001-328425/34.
XX
XX Peptide derivatives, useful as S1 protease inhibitors for modulating
XX expression of genes regulated by SREBP transcription factors and for
XX treating conditions associated with abnormal cholesterol or lipid
XX homeostasis.
XX
XX Example; Page 24; 4lpp; English.
XX
XX The present invention describes a number of peptide derivatives which are
XX capable of modulating Site-1 protease (S1P). S1P initiates the release of
XX sterol regulatory element binding proteins (SREBPs), which control the
XX synthesis of fatty acids and cholesterol. The peptide derivatives of the
XX invention are, therefore, useful in the modulation of cholesterol
XX homeostasis and in the treatment of conditions associated with abnormal
XX levels of plasma cholesterol, lipoproteins or triglycerides. The present
XX sequence is a peptide used in the exemplification of the invention
XX
XX Sequence 4 AA;
XX
XX Query Match 84.2%; Score 16; DB 4; Length 4;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+06;
XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RVKR 4
XX ||:|
XX 1 RVRR 4
XX
XX Db
XX
XX RESULT 6
XX ID AAB97427 standard; peptide; 4 AA.
XX
XX AC AAB97427;
XX
XX 27-JUL-2001 (first entry)
XX
XX Site-1 protease fluorogenic peptide assay substrate #10.
XX
XX Site-1 protease; S1P; sterol regulatory element binding protein; SREBP;
XX fatty acid synthesis; cholesterol homeostasis; triglyceride.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /label= OTHER
FT
FT Modified-site 4 /note= "modified by t-butyloxycarbonyl"
FT
FT /label= OTHER
FT
FT /note= "modified by 4-methyl-coumaryl-7-amide"
FT
FT

```

```

XX PN WO200127138-A2.
XX
XX PD 19-APR-2001.
XX
XX PF 11-OCT-2000; 2000WO-US028428.
XX
XX PR 13-OCT-1999; 99US-0159236P.
XX
XX (TULA-) TULARIK INC.
XX (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
XX
XX Jaen JC, Li L, Brown MS, Goldstein JL, Cheng D;
XX WPI; 2001-328425/34.
XX
XX Peptide derivatives, useful as S1 protease inhibitors for modulating
XX expression of genes regulated by SREBP transcription factors and for
XX treating conditions associated with abnormal cholesterol or lipid
XX homeostasis.
XX
XX Example; Page 27; 4lpp; English.
XX
XX The present invention describes a number of peptide derivatives which are
XX capable of modulating Site-1 protease (S1P). S1P initiates the release of
XX sterol regulatory element binding proteins (SREBPs), which control the
XX synthesis of fatty acids and cholesterol. The peptide derivatives of the
XX invention are, therefore, useful in the modulation of cholesterol
XX homeostasis and in the treatment of conditions associated with abnormal
XX levels of plasma cholesterol, lipoproteins or triglycerides. The present
XX sequence is a peptide substrate of S1P which can be used in a fluorogenic
XX peptide assay of S1P
XX
XX Sequence 4 AA;
XX
XX Query Match 84.2%; Score 16; DB 4; Length 4;
XX Best Local Similarity 75.0%; Pred. No. 1.8e+06;
XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 RVKR 4
XX ||:|
XX 1 RVRR 4
XX
XX Db
XX
XX RESULT 7
XX ID AAE24432 standard; peptide; 4 AA.
XX
XX AC AAE24432;
XX
XX 04-OCT-2002 (first entry)
XX
XX Transporter peptide, T5.
XX
XX Transporter peptide; therapy; colon cancer; neurodegenerative disorder;
XX diabetes; respiratory ailment; cardioplegia; viral infection; cytostatic;
XX virucide; neuroprotective.
XX
XX Unidentified.
XX
XX WO200231109-A2.
XX
XX 18-APR-2002.
XX
XX 15-OCT-2001; 2001WO-IB002423.
XX
XX 13-OCT-2000; 2000US-0240315P.
XX (UYLA-) UNIV LAUSANNE.
XX
XX Bonny C;
XX
XX WPI; 2002-479626/51.
XX
XX

```

XX Novel transporter peptide useful for the intracellular delivery of
 PT biological effectors for treating diabetes, colon cancer, respiratory
 PT ailments, neurodegenerative disorders, cardioplegia, and viral infections.
 XX
 XX
 PS Claim 35; Page 26; 50pp; English.
 XX
 CC The present invention relates to novel transporter peptides with the
 CC capacity to facilitate transport of an effector across a biological
 CC membrane. Sequences of the invention are useful for translocating an
 CC effector into the cytoplasm and nucleus of a eukaryotic cell preferably a
 CC human cell. They are also useful for increasing the intracellular
 CC concentration of an effector within a eukaryotic cell, preferably human
 CC cell. Transporter peptides of the invention are useful for transporting
 CC an effector across a biological membrane, for targeting various cell
 CC types for the intracellular delivery of drugs and therapeutic agents and
 CC for increasing the biological activity of the effector to which it is
 CC coupled. Pharmaceutical compositions comprising the transporter peptides
 CC are useful for treating or preventing diseases such as colon cancer,
 CC diabetes, respiratory ailments, neurodegenerative disorders, cardioplegia
 CC and viral infections. The present sequence is a transporter peptide of
 CC the invention. This peptide can be translocated across a membrane of lung
 CC cells
 XX
 SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVKR 4
 ||:|
 Db 1 RVRK 4

RESULT 8
 AA014861
 ID AAO14861 standard; protein; 4 AA.

XX AAO14861;

XX 19-JUL-2002 (first entry)

DE Purin substrate peptide.

XX Furin substrate; serine protease inhibitor;
 KW serine protease substrate recognition site interaction; emphysema;
 KW respiratory distress syndrome; septic shock; multiple organ failure;
 KW myocardial ischemia; reperfusion injury; dermatitis; cystic fibrosis;
 KW chronic bronchitis; arteriosclerosis; Alzheimer's disease; corneal ulcer;
 KW rheumatoid arthritis; acute pancreatitis.

XX Unidentified.

XX US6358928-B1.

XX 19-MAR-2002.

XX 22-NOV-1999; 99US-00444883.

XX 22-NOV-1999; 99US-00444883.

XX (ENZY-) ENZYME SYST PROD INC.

XX Rasnick DW;

XX WPI; 2002-391718/42.

XX New alpha-amino acid or peptidyl compounds having a C-terminal
 PT imidazolesulfonylmethylene group are useful as serine protease inhibitors
 PT for treatment of e.g. Alzheimer's disease or multiple organ failure.

XX Claim 17; Col 11; 16pp; English.

XX The invention comprises alpha-amino acid and peptidyl compounds having a
 CC C-terminal imidazolesulfonylmethylene group which is a serine protease
 CC inhibitor. The compounds of the invention are capable of interacting with
 CC the substrate recognition site of a serine protease. The compounds of the
 CC invention are useful for the treatment of diseases characterised by over-
 CC activity of one or more serine proteases, e.g. respiratory distress
 CC syndrome; septic shock; multiple organ failure; emphysema; myocardial
 CC ischemia; reperfusion injury; dermatitis; cystic fibrosis; chronic
 CC bronchitis; arteriosclerosis; Alzheimer's disease; corneal ulcers;
 CC rheumatoid arthritis and acute pancreatitis. The present amino acid
 CC sequence represents the furin (serine protease) substrate peptide
 XX

SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RVKR 4
 ||:|
 Db 1 RVRK 4

RESULT 9
 ABP71148
 ID ABP71148 standard; peptide; 4 AA.

XX AC ABP71148;

XX 14-APR-2003 (first entry)

XX Human proneurotrophin cleavage site in BDNF protein.

XX Proneurotrophin; nerve growth factor; NGF; neurotrophin; NT-3; NT4; NT5;
 KW brain derived neurotrophic factor; BDNF; vasotropic; cerebroprotective;
 KW antimicrobial; cardiant; virucide; antibacterial; neuroprotective; MMP;
 KW nootropic; antiinflammatory; anticonvulsant; plasminogen; plasmin; p75;
 KW apoptosis; human.

XX Homo sapiens.

XX WO200296356-A2.

XX 05-DEC-2002.

XX 24-MAY-2002; 2002WO-US016540.

XX 25-MAY-2001; 2001US-0293823P.

XX 13-JUL-2001; 2001US-0305510P.

XX (CORR) CORNELL RES FOUND INC.

XX Hempstead BL, Lee R, Teng KK, Kermani P;

XX WPI; 2003-140406/13.

XX Novel protein for inducing apoptosis, has proneurotrophin pro-domain with
 PT conserved regions, mature neurotrophin domain, and connector that joins
 PT conserved region to mature domain and resistant to protease cleavage.

XX Disclosure; Page 13; 124pp; English.

XX The invention relates to an isolated protein comprising a pro-domain (PD)
 CC of a proneurotrophin, where PD comprises a pro-domain conserved region,
 CC or a modified proneurotrophin protein (Ib) with a PD, a mature
 CC neurotrophin domain (ND), and a connector that joins the pro-domain
 CC conserved region to ND and resistant to protease cleavage. The PD is
 CC selected from specific peptide fragments of human nerve growth factor
 CC (NGF), human brain derived neurotrophic factor (BDNF), human neurotrophin
 CC 3 (NT-3) or human neurotrophin 4/5 (NT4/5). (Ib) is useful for inducing
 CC apoptosis in a cell comprising p75 receptors (normal number or higher
 CC than the normal number of p75 receptors) on its surface, by causing the

CC p75 receptor to bind (Ib), in vitro, in mammals or humans. The method is
 CC useful for treating vascular smooth muscle plaque e.g. atherosclerotic
 CC plaque. The cell is a malignant cell e.g. cells of tumour, melanoma,
 CC prostate, pancreas, nervous system (e.g. medulloblastoma or astrocytoma),
 CC leukemia, lymphoma, testicular, lung, brain, malignant oligodendrocyte,
 CC heart, vascular smooth muscle or neural cell. A molecule that inhibits
 CC the binding of pronurotrophin to a p75 receptor is useful in a method
 CC for inhibiting apoptosis of a cell in a mammal e.g. human suffering from
 CC a condition associated with undesired apoptosis due to binding of a
 CC pronurotrophin to p75 receptor. The condition is the result of an injury
 CC or an environmental insult, e.g. nervous system injury, caused by a
 CC chemical or radiation or occurring during cancer treatment, hypoxic
 CC ischaemia caused by stroke or heart attack, viral or microbial infection,
 CC meningitis, encephalitis or abscesses, neurodegenerative disorders e.g.
 CC Alzheimer's disease, familial dysautonomia, ataxia telangiectasia,
 CC Charcot-Marie-Tooth disease, Adreno leuko dystrophy, spinal muscular
 CC atrophy or Friedreich's ataxia, or multiple sclerosis, convulsions,
 CC epilepsy and spinal cord injury. The present sequence represents the
 CC human pronurotrophin cleavage site in BDNF protein
 XX
 CC Sequence 4 AA;

Query Match 84.2%; Score 16; DB 6; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:|
 Db 1 RVRR 4

RESULT 10
 ADA10587
 ID ADA10587 standard; peptide; 4 AA.

XX ADA10587;

AC 06-NOV-2003 (first entry)

XX Eglin c variant related fluorogenic substrate.

XX protease inhibitor; eglin c variant; reactive loop; acute bacterial;
 XX viral; fungal; infection; blocking endoproteolytic activation;
 KW bacterial toxin; anthrax toxin protective antigen; diphtheria toxin;
 KW Pseudomonas aeruginosa exotoxin A; shiga toxin; transgenic animal;
 KW fluorogenic; substrate.

XX Unidentified.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "Modified by Boc"

FT Modified-site 4 /note= "Modified by MCA"

FT WO2002102318-A2.

XX 27-DEC-2002.

XX 18-JUN-2002; 2002WO-US019394.

XX 18-JUN-2001; 2001US-0299096P.

PR 17-JUN-2002; 2002US-00299096.

XX (UNMI) UNIV MICHIGAN.

XX Komiyama T, Fuller RS;

XX WPI; 2003-167438/16.

XX Composition useful for treating diseases including acute bacterial, viral
 PT and fungal infections, has protease inhibitor that is eglin c variant
 PT having a non-naturally occurring amino acid in adventitious contact site.

XX Example 1; Page 76; 112pp; English.

XX This invention relates to a novel composition comprising a protease
 CC inhibitor that is an eglin c variant comprising at least one non-
 CC naturally occurring amino acid in an adventitious contact site, and
 CC further comprising at least one non-naturally occurring amino acid in a
 CC reactive loop. The novel composition is useful for treating disease
 CC including acute bacterial (e.g. Bacillus anthracis, Corynebacterium
 CC diphtheriae, and Pseudomonas aeruginosa), viral (respiratory syncytial
 CC virus, measles virus, and human immunodeficiency virus) and fungal
 CC (candidiasis and pneumocystis pneumonia) infections in a patient exposed
 CC to an infectious agent. The eglin c variants are useful for blocking
 CC endoproteolytic activation of a bacterial toxin including anthrax toxin A
 CC protective antigen, diphtheria toxin, Pseudomonas aeruginosa exotoxin A
 CC and shiga toxin. The eglin c variants are also useful as affinity
 CC purification reagents, as fluorescence tags for identification of cells
 CC containing target proteases, for subcellular localisation of proteases,
 CC and for tracking internalisation of drugs and for examining and
 CC inhibiting physiological functions of processing or other proteases in
 CC cell cultures or in transgenic animals, for example by selectively
 CC inhibiting the enzymes. The eglin c variants are small, stable and
 CC reversible. This sequence represents a fluorescent substrate peptide used
 CC in the creation of first generation eglin c variants of the invention.

XX Sequence 4 AA;

Query Match 84.2%; Score 16; DB 6; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:|
 Db 1 RVRR 4

RESULT 11

ADD84924

ID ADD84924 standard; peptide; 4 AA.

XX ADD84924;

XX 29-JAN-2004 (first entry)

DT Tetrapeptide protease-sensitive linker SEQ ID NO:19.

DE molecular adjuvant; nicotine hapten; antiaddictive; vaccine; nicotine;
 XX smoking; nicotine addiction; immunisation.

XX Synthetic.

XX WO2003082329-A2.

XX 09-OCT-2003.

XX 20-FEB-2003; 2003WO-US005015.

XX 01-MAR-2002; 2002US-0360967P.

XX (UYNE-) UNIV NEBRASKA.

PA (SAND/) SANDERSON S D G.

PA (VENN/) VENNSTROM J L.

PA (THIE/) THIELE G M.

PA (PARA/) PARAMESWARAN M.

PA (BEVI/) BEVINS R A.

PA (SRIN/) SRINIVASA C R.

XX Sanderson SDG, Vennstrom JL, Thiele GM, Parameswaran M;

PI Bevins RA, Srinivasa CR;

XX WPI; 2003-902908/82.

XX Compound useful as nicotine vaccine comprises molecular adjuvant with

PT targeting ligand linked to nicotine hapten.

XX Example 5; SEQ ID NO 19; 90pp; English.

XX The present invention describes a compound (I) comprising a molecular

CC adjuvant linked to a nicotine hapten. The molecular adjuvant comprises a

CC targeting ligand having binding affinity for an antigen presenting cell.

CC The targeting ligand is functionally linked to the nicotine hapten so

CC that the binding of the molecular adjuvant to the antigen presenting cell

CC determinant activates the antigen presenting cell and effecting delivery

CC of the nicotine hapten to an antigen presenting pathway. Also described

CC is a method for the preparation of antibodies to a nicotine hapten

CC involving: (a) immunising an animal with (I); (b) isolating antibodies

CC from the sera of the animal; and (c) recovering the isolated antibodies.

CC (I) has antiaddictive activities, and can be used in vaccines. (I) can be

CC used for the treatment or prevention of nicotine addiction via

CC immunisation with a nicotine vaccine. The compound (I) is capable of

CC causing smoking cessation and long term compliance; and delivers both

CC stimulatory signals and the nicotine antigen to antigen presenting cells

CC (APCs), and so inducing an anti-nicotine antibody response with little or

CC no inflammatory side effects and without reliance on other added

CC adjuvants. The present sequence is used in the exemplification of the

CC present invention.

XX Sequence 4 AA;

SEQ

Query Match 84.2%; Score 16; DB 7; Length 4;

Best Local Similarity 75.0%; Pred. NO. 1.8e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4

DB ||:|

1 RVRR 4

RESULT 12

ADG19004

ID ADG19004 standard; peptide; 4 AA.

XX

AC ADG19004;

XX

DT 11-MAR-2004 (first entry)

XX

DE Multimeric transporter peptide related peptide SEQ ID NO:29.

XX

KW multimetric transporter peptide; transporter peptide; antidiabetic;

XX cytosolic; antiinflammatory; nontropic; neuroprotective; virucide;

KW gene therapy; diabetes; colon cancer; respiratory ailment;

KW neurodegenerative disorder; cardioplegia; viral infection.

XX

OS Synthetic.

XX

PN WO2003103718-A2.

XX

PD 18-DEC-2003.

XX

PF 06-JUN-2003; 2003WO-IB003097.

XX

PR 07-JUN-2002; 2002US-00165015.

XX

PA (UYLA-) UNIV LAUSANNE.

XX

PI Bonny C;

XX

DR WPI; 2004-062229/06.

XX

XX New multimeric transporter peptides, useful for treating diabetes, colon

PT cancer, respiratory ailments, neurodegenerative disorders, cardioplegia,

PT and viral infections.

XX

PS Claim 3; SEQ ID NO 29; 49pp; English.

XX

CC The present invention describes a multimeric transporter peptide (I).

CC Also described: (1) a transporter unit comprising the transporter peptide

CC and an effector; (2) translocating the transporter unit across the

CC membrane of pancreatic beta-cells, hepatocytes, muscle cells or lung

CC cells; (3) a pharmaceutical composition comprising the transporter unit

CC and a carrier; (4) a method of producing a translocatable conjugate

CC between the transporter peptide and an effector; (5) a method of

CC increasing the intracellular concentration of an effector with a

CC eukaryotic cell; (6) a kit comprising in one or more containers, the

CC pharmaceutical composition described above; and (7) a method of treating

CC or preventing a disease. (I) has antidiabetic, cytostatic,

CC antiinflammatory, nontropic, neuroprotective and virucide activities, and

CC can be used in gene therapy. The multimeric transporter peptide (I),

CC compositions and methods of the present invention can be used for

CC treating diabetes, colon cancer, respiratory ailments, neurodegenerative

CC disorders, cardioplegia, and viral infections. The present sequence

CC represents a peptide which can be used as part of a multimeric

CC transporter peptide of the present invention.

XX Sequence 4 AA;

SEQ

Query Match 84.2%; Score 16; DB 8; Length 4;

Best Local Similarity 75.0%; Pred. NO. 1.8e+06;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4

DB ||:|

1 RVRR 4

RESULT 13

ADJ57390

ID ADJ57390 standard; peptide; 4 AA.

XX

AC ADJ57390;

XX

DT 06-MAY-2004 (first entry)

XX

DE Peptide fragment of alpha-1-antitrypsin, use as convertase inhibitor.

XX

KW Convertase; inhibitor; alpha-1-antitrypsin; antiinflammatory; vulnery;

XX ophthalmological; dermatological; nephrotropic; hepatotropic; vasotropic;

KW antiinfertility; respiratory-gen.; cardiant; CNS-gen.; cerebroprotective;

KW neuroprotective; nontropic; cytostatic; antiarthritic;

KW antiarteriosclerotic.

XX

OS Unidentified.

XX

PN WO2004009113-A1.

XX

PD 29-JAN-2004.

XX

PF 23-JUL-2003; 2003WO-GB003159.

XX

PR 24-JUL-2002; 2002GB-00017136.

XX

PA (RENO-) RENOVO LTD.

XX

PI Ferguson MWJ, Brunner G;

XX

DR WPI; 2004-180270/17.

XX

PT Use of a convertase inhibitor in the manufacture of a medicament for

PT reducing scarring during the healing of wounds or reducing fibrosis in

PT the treatment of fibrotic conditions.

XX

PS Disclosure; Page 10; 43pp; English.

XX

CC The present sequence is that of a peptide fragment of alpha-1-

CC antitrypsin. Convertase inhibitors of the invention may be derivatives of

CC alpha-1-antitrypsin comprising this sequence. The inventors have

CC established that convertase enzymes act, both extracellularly and

CC intracellularly, to cause the activation of latent transforming growth

CC factor-beta (TGF-beta) in the extracellular space at the site of a wound

CC of a fibrotic conditions. Thus, the present invention relates to use of
 CC convertase inhibitors for the reduction of scarring during the healing of
 CC wounds, for reducing fibrosis in the treatment of fibrotic conditions,
 CC for treating wounds to prevent scar formation, for preventing scarring of
 CC the eye, nervous tissue or intestines, dermal scarring and scarring
 CC following a burn. The fibrotic condition is a fibrotic disorder such as
 CC glomerulonephritis, cirrhosis of the liver, fibrotic disease, adhesions
 CC and restenosis (all claimed). The convertase inhibitor can also be used
 CC for the treatment of hypertrophic and keloid scars, scarring in the heart,
 CC scarring of the gut, scarring in the pelvis in the region of the
 CC fallopian tubes leading to infertility, scarring following injury to the
 CC muscles, scarring or fibrosis following injury to tendons and ligaments,
 CC which can result in serious loss of function, liver fibrosis, pulmonary
 CC fibrosis, scleroderma, myocardial hibernation, fibrosis following a
 CC myocardial infarction, central nervous system fibrosis following a stroke
 CC or neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
 CC vitreoretinopathy, arthritis, arteriosclerosis and cancer.
 XX
 SQ Sequence 4 AA;

Query Match 84.2%; Score 16; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:
 1 RVKR 4

RESULT 14

ID AAR37629
 ID AAR37629 standard; protein; 4 AA.

XX AAR37629;

XX 25-MAR-2003 (revised)

DT 24-SEP-1993 (first entry)

XX Sequence of proinsulin variant proins.RTKR.Ip having a non-naturally
 DE occurring prohormone convertase cleavage site.

XX Prohormone convertase; enzyme; cleavage; proinsulin; hormone.

XX Synthetic.

XX WO9311247-A1.

XX 10-JUN-1993.

XX 04-DEC-1992; 92WO-US010621.

XX 06-DEC-1991; 91US-00803631.

XX 22-MAY-1992; 92US-00887265.

XX (GETH) GENENTECH INC.

XX Gorman CM, Groskreutz DJ, Marriott D;

XX WPI; 1993-197065/24.

XX Heterologous polypeptide factor prepn. - by introducing into polypeptide
 PT factor dependent host cell nucleic acid, and then culturing host cell,
 PT etc.

XX Example; Page 56; 134pp; English.

XX The inventors describe the production of mammalian cells expressing
 CC prohormone convertase which facilitates the processing of prohormone
 CC precursors to active hormones. More specifically the cleavage site is the
 CC prohormone convertase cleavage site given in AAR37632-35. A human
 CC proinsulin mutant having a non-naturally occurring prohormone convertase
 CC cleavage site is constructed by mutating the human proinsulin cDNA,
 CC pRK.proins encoding the naturally occurring basic cleavage site at the B-

CC chain/C-peptide junction (AAR37627) and/or A-chain/C-peptide junction
 CC (AAR37628) by site-directed mutagenesis (Kunkel 1987). The following
 CC proinsulin variants were constructed: proins.RTKR.Ip, proins.RQKR.IIp and
 CC proins.KTKR.Ip (see AAR37629-31). The following double proinsulin
 CC variants were constructed: proins.KR.Ip/RQKR.IIp and
 CC proins.RTKR.Ip/RQKR.IIp. Primers used in proinsulin mutant construction
 CC were AAQ43265-67. (Updated on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 4 AA;

Query Match 78.9%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
 ||:
 1 RVKR 4

RESULT 15

AAR60593

ID AAR60593 standard; peptide; 4 AA.

XX AAR60593;

XX 25-MAR-2003 (revised)

DT 27-APR-1995 (first entry)

XX proins.RTKR.Ip proinsulin mutant cleavage site.

XX prohormone; convertase; insulin; proinsulin; proproinsulin; factor;

KW growth; precursors; transgenic; mammal; pcr; primer.

XX Synthetic.

XX WO9420624-A1.

XX 15-SEP-1994.

XX 01-MAR-1994; 94WO-US002233.

XX 01-MAR-1993; 93US-00026143.

XX (GETH) GENENTECH INC.

XX Gorman CM, Groskreutz DJ;

XX WPI; 1994-303031/37.

XX Treating insulin-dependent disorders in mammals - by introducing a
 PT nucleic acid encoding a variant proinsulin into a host cell with a
 PT constitutive pathway of protein secretion, or a plasmid, and introducing
 PT the cell or plasmid to the mammal.

XX Example 4; Page 54; 117pp; English.

XX The cDNA clone of the human proinsulin gene, pSVEHIGDHP, was
 CC amplified by primers AAQ71463-4 in a RACE-PCR. The product was ligated in
 CC plasmid pRK5 and called pRK.proins. Mutants of the prohormone convertase
 CC (PC) cleavage site in the human proinsulin were constructed (AAR60591-
 CC 5) The mutated sites are specifically recognised by murine PC. The new
 CC cleavage sites are labelled either Ip or Iip. Ip is a Type I enzyme
 CC cleavage site whereas Iip is a Type II enzyme cleavage site. Cells
 CC containing both the prohormone convertase gene and the required precursor
 CC gene e.g proproinsulin to be expressed can be injected into a mammal.
 CC This system can be used to treat insulin-responsive disorders. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX

SQ Sequence 4 AA;

Query Match 78.9%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RVKR 4
| |
Db 1 RTRK 4

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OM protein - protein search, using sw model

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 12390

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	16	84.2	4	1	US-08-002-202-4
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3	16	84.2	4	1	US-08-460-343B-73
4	16	84.2	4	1	US-08-398-028B-73
5	16	84.2	4	2	US-08-504-265B-73
6	16	84.2	4	3	US-08-481-534-4
7	16	84.2	4	3	US-08-481-534-20
8	16	84.2	4	3	US-08-753-247-29
9	16	84.2	4	3	US-09-360-237-40
10	16	84.2	4	3	US-09-360-237-54
11	16	84.2	4	3	US-09-444-883-3
12	16	84.2	4	4	US-09-640-198D-33
13	16	84.2	4	4	US-09-639-667-3
14	15	78.9	4	1	US-08-200-900A-36
15	15	78.9	4	1	US-08-200-900A-38
16	15	78.9	4	2	US-08-504-265B-86
17	15	78.9	4	2	US-08-545-562A-65
18	15	78.9	4	3	US-08-026-143B-22
19	15	78.9	4	3	US-09-537-696-23
20	15	78.9	4	4	US-09-626-896-23
21	15	78.9	4	4	US-09-601-040A-21
22	15	78.9	4	4	US-08-794-042-36
23	15	78.9	4	4	US-08-794-042-38
24	15	78.9	4	5	PCT-US92-10621-22
25	15	78.9	4	5	PCT-US94-02233-22
26	15	78.9	4	5	PCT-US94-07779-16
27	14	73.7	4	2	US-08-323-686-23

28	14	73.7	4	2	US-08-595-043A-15	Sequence 15, Appl
29	14	73.7	4	3	US-08-651-472-74	Sequence 14, Appl
30	14	73.7	4	3	US-09-000-041A-14	Sequence 74, Appl
31	14	73.7	4	3	US-08-358-928-74	Sequence 74, Appl
32	14	73.7	4	3	US-09-391-104-33	Sequence 33, Appl
33	14	73.7	4	4	US-09-185-852-11	Sequence 11, Appl
34	14	73.7	4	4	US-09-640-198D-7	Sequence 7, Appl
35	14	73.7	4	4	US-09-639-667-5	Sequence 5, Appl
36	14	73.7	4	4	US-09-323-738-11	Sequence 11, Appl
37	14	73.7	4	4	US-09-734-002-14	Sequence 14, Appl
38	13	68.4	4	1	US-08-088-322-5	Sequence 5, Appl
39	13	68.4	4	1	US-08-002-202-1	Sequence 1, Appl
40	13	68.4	4	1	US-08-002-202-2	Sequence 2, Appl
41	13	68.4	4	1	US-08-002-202-3	Sequence 3, Appl
42	13	68.4	4	1	US-08-437-820-5	Sequence 5, Appl
43	13	68.4	4	1	US-08-664-856A-7	Sequence 7, Appl
44	13	68.4	4	1	US-08-082-849B-32	Sequence 32, Appl
45	13	68.4	4	1	US-08-368-852-6	Sequence 6, Appl
46	13	68.4	4	1	US-08-801-796-7	Sequence 7, Appl
47	13	68.4	4	1	US-08-443-568B-40	Sequence 40, Appl
48	13	68.4	4	2	US-08-115-519-1	Sequence 1, Appl
49	13	68.4	4	2	US-08-931-877-7	Sequence 7, Appl
50	13	68.4	4	2	US-08-545-562A-66	Sequence 66, Appl
51	13	68.4	4	2	US-08-373-190-56	Sequence 56, Appl
52	13	68.4	4	2	US-08-525-940-6	Sequence 6, Appl
53	13	68.4	4	2	US-08-476-014-1	Sequence 1, Appl
54	13	68.4	4	2	US-08-595-043A-39	Sequence 39, Appl
55	13	68.4	4	2	US-08-438-190A-56	Sequence 56, Appl
56	13	68.4	4	2	US-08-976-838-6	Sequence 6, Appl
57	13	68.4	4	3	US-08-350-215-58	Sequence 58, Appl
58	13	68.4	4	3	US-09-069-484-7	Sequence 7, Appl
59	13	68.4	4	3	US-08-481-534-1	Sequence 1, Appl
60	13	68.4	4	3	US-08-481-534-2	Sequence 2, Appl
61	13	68.4	4	3	US-08-481-534-3	Sequence 3, Appl
62	13	68.4	4	3	US-09-287-145A-56	Sequence 56, Appl
63	13	68.4	4	3	US-08-641-873-13	Sequence 13, Appl
64	13	68.4	4	3	US-07-956-483-1	Sequence 1, Appl
65	13	68.4	4	3	US-08-472-240A-21	Sequence 21, Appl
66	13	68.4	4	3	US-09-369-744-7	Sequence 7, Appl
67	13	68.4	4	3	US-09-556-111-56	Sequence 56, Appl
68	13	68.4	4	3	US-08-065-844A-17	Sequence 17, Appl
69	13	68.4	4	3	US-08-026-143B-23	Sequence 23, Appl
70	13	68.4	4	3	US-09-537-696-19	Sequence 19, Appl
71	13	68.4	4	3	US-09-391-104-9	Sequence 9, Appl
72	13	68.4	4	4	US-09-475-515-23	Sequence 23, Appl
73	13	68.4	4	4	US-09-368-630-11	Sequence 11, Appl
74	13	68.4	4	4	US-09-368-630-16	Sequence 16, Appl
75	13	68.4	4	5	PCT-US92-10621-23	Sequence 23, Appl
76	13	68.4	4	5	PCT-US94-02233-23	Sequence 23, Appl
77	13	68.4	4	5	PCT-US94-07779-17	Sequence 17, Appl
78	12	63.2	4	1	US-07-998-972A-34	Sequence 34, Appl
79	12	63.2	4	1	US-08-463-953-34	Sequence 34, Appl
80	12	63.2	4	1	US-08-462-261-34	Sequence 34, Appl
81	12	63.2	4	1	US-08-002-202-10	Sequence 10, Appl
82	12	63.2	4	2	US-08-504-265B-87	Sequence 87, Appl
83	12	63.2	4	2	US-08-756-506-20	Sequence 20, Appl
84	12	63.2	4	3	US-08-481-534-10	Sequence 10, Appl
85	12	63.2	4	3	US-08-481-534-15	Sequence 15, Appl
86	12	63.2	4	3	US-07-956-483-2	Sequence 2, Appl
87	12	63.2	4	3	US-08-472-240A-22	Sequence 22, Appl
88	12	63.2	4	3	US-08-026-143B-24	Sequence 24, Appl
89	12	63.2	4	4	US-08-171-384A-1	Sequence 1, Appl
90	12	63.2	4	4	US-09-627-851B-25	Sequence 25, Appl
91	12	63.2	4	5	PCT-US91-02766-3	Sequence 3, Appl
92	12	63.2	4	5	PCT-US92-10621-24	Sequence 24, Appl
93	12	63.2	4	5	PCT-US92-11357-34	Sequence 34, Appl
94	12	63.2	4	5	PCT-US94-02233-24	Sequence 24, Appl
95	11	57.9	4	1	US-08-079-812-10	Sequence 10, Appl
96	11	57.9	4	1	US-08-079-812-22	Sequence 22, Appl
97	11	57.9	4	1	US-08-336-343A-20	Sequence 20, Appl
98	11	57.9	4	1	US-08-426-819A-23	Sequence 23, Appl
99	11	57.9	4	1	US-08-808-641-13	Sequence 13, Appl
100	11	57.9	4	2	US-08-025-321C-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-08-002-202-4
; Sequence 4, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Purin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Modified-sites
; OTHER INFORMATION: /note= "The amino terminus is derivatized by a
; OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus is
; OTHER INFORMATION: derivatized by a 4-methylcoumaryl-7-amide group;"
US-08-002-202-4

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVRR 4

RESULT 2
US-08-002-202-20
; Sequence 20, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Purin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
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; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1..4
; OTHER INFORMATION: /label= Modified-sites
; OTHER INFORMATION: /note= "The amino terminus is derivatized by a
; OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus is
; OTHER INFORMATION: derivatized by a 4-methylcoumaryl-7-amide group;"
US-08-002-202-20

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVRR 4

RESULT 3
US-08-460-343B-73
; Sequence 73, Application US/08460343B
; Patent No. 5741664
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,343B
; FILING DATE: 01-Jun-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398028
; FILING DATE: 03-mar-1995
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; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0936C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-460-343B-73

Query Match      84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVRK 4
      ||:|
Db      1 RVRK 4

RESULT 4
US-08-398-028B-73
; Sequence 73, Application US/08398028B
; Patent No. 5780285
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITISIN VARIANTS CAPABLE OF CLEAVING
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; FILING DATE: 03-Mar-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398028
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0936P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8228
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-504-265B-73

Query Match      84.2%; Score 16; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVRK 4
      ||:|
Db      1 RVRK 4

RESULT 6
US-08-481-534-4
; Sequence 4, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and reagents for inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-481-534-4

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
Db      1 RVRR 4

RESULT 7
US-08-481-534-20
/ Sequence 20, Application US/08481534
/ Patent No. 6022855
/ GENERAL INFORMATION:
/ APPLICANT: Thomas, Gary
/ APPLICANT: Anderson, Eric D
/ APPLICANT: Thomas, Laurel
/ APPLICANT: Haylick, Joel S
/ APPLICANT: Nelson, Jay
/ APPLICANT: Stenglen, Stephan G
/ TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
/ TITLE OF INVENTION: Endoprotease
/ NUMBER OF SEQUENCES: 21
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: IL
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid

/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/481,534
/ FILING DATE: 14-SEP-1995
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6022855nan, Kevin E
/ REGISTRATION NUMBER: 35,303
/ REFERENCE/DOCKET NUMBER: 92,448-D
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-913-0001
/ TELEFAX: 312-913-0002
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid

/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ NAME/KEY: Modified site
/ LOCATION: 1..4
/ OTHER INFORMATION: /label=Modified site
/ OTHER INFORMATION: /note="The amino terminus us derivatized by a
/ OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus
/ OTHER INFORMATION: is derivatized by a 4-methylcoumaryl-7-amide group."
US-08-481-534-20

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 RVKR 4
Db      1 RVRR 4

RESULT 8
US-08-753-247-29
/ Sequence 29, Application US/08753247
/ Patent No. 6210929
/ GENERAL INFORMATION:
/ APPLICANT: SCHLOKAT, Uwe
/ APPLICANT: FISCHER, Bernhard
/ APPLICANT: FALKNER, Falko-Guenther
/ APPLICANT: DORNER, Friedrich
/ APPLICANT: EIBL, Johann
/ TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
/ TITLE OF INVENTION: DERIVATIVE OR A DERIVATIVE OF A FURIN ANALOGUE AND A
/ TITLE OF INVENTION: HETEROLOGOUS SEQUENCE
/ NUMBER OF SEQUENCES: 29
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Foley & Lardner
/ STREET: 3000 K Street, N.W., Suite 500
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20007-5109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/753,247
/ FILING DATE: 22-NOV-1996
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: AT 1928/95
/ FILING DATE: 24-NOV-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 40433/149
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 29:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 4 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
US-08-753-247-29

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

RESULT 9
US-09-360-237-40
; Sequence 40, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-40

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

RESULT 10
US-09-360-237-54
; Sequence 54, Application US/09360237
; Patent No. 6322962
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: CHENG, DONG
; APPLICANT: ESPENSHADE, PETER J.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: RAWSON, ROBERT B.
; APPLICANT: SAKAI, JURO
; TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF
; TITLE OF INVENTION: MODULATORS THEREOF
; FILE REFERENCE: UTXD:567
; CURRENT APPLICATION NUMBER: US/09/360,237
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: 60/096,571
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-360-237-54

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

RESULT 11
US-09-444-883-3
; Sequence 3, Application US/09444883
; Patent No. 6358928
; GENERAL INFORMATION:
; APPLICANT: Rasmick, David W.
; TITLE OF INVENTION: PEPTIDYL SULFONYL IMIDAZOLIDES AS SELECTIVE INHIBITORS OF
; TITLE OF INVENTION: SERINE PROTEASES
; FILE REFERENCE: 6095-5
; CURRENT APPLICATION NUMBER: US/09/444,883
; CURRENT FILING DATE: 1999-11-22
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Binding Site for Furin
US-09-444-883-3

Query Match      84.2%; Score 16; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

RESULT 12
US-09-640-198D-33
; Sequence 33, Application US/09640198D
; Patent No. 6586411
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen
; APPLICANT: Kay Whye, Peng
; TITLE OF INVENTION: System for Monitoring the Location of
; TITLE OF INVENTION: Transgenes
; FILE REFERENCE: 07039-295001
; CURRENT APPLICATION NUMBER: US/09/640,198D
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Cleavable Linker Site
US-09-640-198D-33

Query Match      84.2%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

QY      1 RVKR 4
      ||:|
Db      1 RVRR 4

Best Local Similarity 75.0%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

RESULT 13
US-09-639-667-3
; Sequence 3, Application US/09639667
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; Patent No. 6632800
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen James
; APPLICANT: Peng, Kan Miye
; TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
; FILE REFERENCE: 07039-292001
; CURRENT APPLICATION NUMBER: US/09/639,667
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: linker peptide
US-09-639-667-3

Query Match 84.2%; Score 16; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RLKR 4

RESULT 14
US-08-200-900A-36
; Sequence 36, Application US/08200900A
; Patent No. 5665566
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,900A
; FILING DATE: 23-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, Maureen C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5201-FWC
; TELEPHONE: (617) 876-1170 X8574
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-200-900A-36

Query Match 78.9%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 15
US-08-200-900A-38
; Sequence 38, Application US/08200900A
; Patent No. 5665566
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/200,900A
; FILING DATE: 23-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meinert, Maureen C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5201-FWC
; TELEPHONE: (617) 876-1170 X8574
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-200-900A-38

Query Match 78.9%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

Search completed: June 20, 2005, 16:35:40
Job time : 30 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:33:52 ; Search time 104 Seconds
(without alignments)
14.768 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1714042 seqs, 383979560 residues

Total number of hits satisfying chosen parameters: 11248

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Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	19	100.0	4	16	US-10-478-179-8
3	16	84.2	4	9	US-09-977-831-29
4	16	84.2	4	14	US-10-165-015-29
5	16	84.2	4	14	US-10-155-886-24
6	16	84.2	4	15	US-10-428-868-33
7	16	84.2	4	16	US-10-399-127-29
8	16	84.2	4	16	US-10-641-834-3
9	15	78.9	4	9	US-09-887-669-12
10	15	78.9	4	9	US-09-841-730-23
11	15	78.9	4	10	US-09-997-868-22
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					Sequence 8, Appli
					Sequence 29, Appli
					Sequence 24, Appli
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					Sequence 12, Appli
					Sequence 23, Appli
					Sequence 22, Appli

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13	15	78.9	4	13	US-10-074-956-26	Sequence 26, Appli
14	15	78.9	4	15	US-10-115-134-60	Sequence 60, Appli
15	15	78.9	4	17	US-10-831-302-15	Sequence 15, Appli
16	15	78.9	4	17	US-10-831-304-38	Sequence 38, Appli
17	15	78.9	4	17	US-10-942-581-5	Sequence 5, Appli
18	14	73.7	4	9	US-09-734-002-14	Sequence 14, Appli
19	14	73.7	4	9	US-09-391-104-33	Sequence 33, Appli
20	14	73.7	4	9	US-09-813-653-11	Sequence 11, Appli
21	14	73.7	4	14	US-10-328-813-11	Sequence 11, Appli
22	14	73.7	4	14	US-10-045-612A-23	Sequence 23, Appli
23	14	73.7	4	15	US-10-057-620-17	Sequence 17, Appli
24	14	73.7	4	15	US-10-428-868-7	Sequence 7, Appli
25	14	73.7	4	15	US-10-215-272-34	Sequence 34, Appli
26	14	73.7	4	16	US-10-716-326-34	Sequence 34, Appli
27	14	73.7	4	16	US-10-641-834-5	Sequence 5, Appli
28	14	73.7	4	17	US-10-715-976-34	Sequence 34, Appli
29	13	68.4	4	9	US-09-391-104-9	Sequence 9, Appli
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32	13	68.4	4	9	US-09-874-736-7	Sequence 7, Appli
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37	13	68.4	4	13	US-10-061-395-43	Sequence 43, Appli
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39	13	68.4	4	14	US-10-155-886-23	Sequence 23, Appli
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41	13	68.4	4	14	US-10-286-332A-11	Sequence 11, Appli
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43	13	68.4	4	14	US-10-358-627-16	Sequence 16, Appli
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45	13	68.4	4	15	US-10-387-336-23	Sequence 23, Appli
46	13	68.4	4	15	US-10-057-620-10	Sequence 10, Appli
47	13	68.4	4	15	US-10-215-272-38	Sequence 38, Appli
48	13	68.4	4	16	US-10-726-422-7	Sequence 7, Appli
49	13	68.4	4	16	US-10-399-127-16	Sequence 16, Appli
50	13	68.4	4	16	US-10-471-220-27	Sequence 27, Appli
51	13	68.4	4	16	US-10-716-326-38	Sequence 38, Appli
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53	13	68.4	4	16	US-10-280-915-11	Sequence 11, Appli
54	13	68.4	4	17	US-10-808-187-1178	Sequence 1178, Ap
55	13	68.4	4	17	US-10-868-381-19	Sequence 19, Appli
56	13	68.4	4	17	US-10-823-259-17	Sequence 17, Appli
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58	13	68.4	4	17	US-10-506-651-30	Sequence 30, Appli
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63	12	63.2	4	10	US-09-882-781-22	Sequence 22, Appli
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65	12	63.2	4	14	US-10-155-886-25	Sequence 25, Appli
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67	12	63.2	4	15	US-10-612-090-5	Sequence 5, Appli
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72	12	63.2	4	19	US-11-016-922-23	Sequence 23, Appli
73	11	57.9	4	10	US-09-852-910-153	Sequence 26, Appli
74	11	57.9	4	14	US-10-197-000-3	Sequence 3, Appli
75	11	57.9	4	15	US-10-057-620-18	Sequence 18, Appli
76	11	57.9	4	15	US-10-245-871-3	Sequence 3, Appli
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78	11	57.9	4	15	US-10-245-871-801	Sequence 801, App
79	11	57.9	4	15	US-10-215-272-35	Sequence 35, Appli
80	11	57.9	4	15	US-10-411-336A-153	Sequence 153, App
81	11	57.9	4	15	US-10-253-286-3	Sequence 3, Appli
82	11	57.9	4	15	US-10-253-286-8	Sequence 8, Appli
83	11	57.9	4	15	US-10-253-286-801	Sequence 801, App
84	11	57.9	4	15	US-10-253-286-801	Sequence 801, App

85 11 57.9 4 16 US-10-751-699-82 Sequence 82, Appl
86 11 57.9 4 16 US-10-716-326-35 Sequence 35, Appl
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88 11 57.9 4 16 US-10-841-787-1 Sequence 1, Appl
89 11 57.9 4 16 US-10-841-787-3 Sequence 3, Appl
90 11 57.9 4 16 US-10-795-676-63 Sequence 63, Appl
91 11 57.9 4 16 US-10-841-056-12 Sequence 12, Appl
92 11 57.9 4 16 US-10-841-121-12 Sequence 12, Appl
93 11 57.9 4 17 US-10-433-709-12 Sequence 12, Appl
94 11 57.9 4 17 US-10-715-976-35 Sequence 35, Appl
95 10 52.6 2 18 US-10-503-910-38 Sequence 38, Appl
96 10 52.6 3 10 US-09-852-910-154 Sequence 154, App
97 10 52.6 3 14 US-10-227-110-18 Sequence 18, Appl
98 10 52.6 3 14 US-10-208-508-18 Sequence 18, Appl
99 10 52.6 3 15 US-10-411-336A-154 Sequence 154, App
100 10 52.6 3 15 US-10-363-112-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-885-914B-3
; Sequence 3, Application US/09885914B
; Publication No. US20040127396A1
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Claire
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885,914B
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213,995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Arg at position 4 is modified at its carboxyl group with a -CH2Cl
US-09-885-914B-3

Query Match 100.0%; Score 19; DB 11; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 2
US-10-478-179-8
; Sequence 8, Application US/10478179
; Publication No. US20040249126A1
; GENERAL INFORMATION:
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: CHEMIC ANTIGEN-SPECIFIC T
; FILE REFERENCE: 07039-277US1
; CURRENT APPLICATION NUMBER: US/10/478,179

; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15992
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/291,874
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker peptide
US-10-478-179-8

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Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 3
US-09-977-831-29
; Sequence 29, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-29

Query Match 84.2%; Score 16; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

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; Sequence 29, Application US/10165015
; Publication No. US20030032594A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 CIP
; CURRENT APPLICATION NUMBER: US/10/165,015
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/977,831
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-10-165-015-29

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Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RVKR 4
DB      1 RVRR 4

RESULT 5
US-10-155-886-24
; Sequence 24, Application US/10155886
; Publication No. US20030087804A1
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence No. US20030087804A1. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-155-886-24

Query Match      84.2%; Score 16; DB 14; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RVKR 4
DB      1 RVRR 4

US-10-428-868-33
; Sequence 33, Application US/10428868
; Publication No. US20030235532A1
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen
; APPLICANT: Kay Whye, Peng
; TITLE OF INVENTION: System for Monitoring the Location of
; TITLE OF INVENTION: Transgenes
; FILE REFERENCE: 07039-295001
; CURRENT APPLICATION NUMBER: US/10/428,868
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/640,198D
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Cleavable Linker Site
US-10-428-868-33

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Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RVKR 4
DB      1 RVRR 4

US-10-641-834-3
; Sequence 3, Application US/10641834
; Publication No. US20040209830A1
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen James
; APPLICANT: Peng, Kah Whye
; TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
; TITLE OF INVENTION: TRANSGENES
; FILE REFERENCE: 07039-292002
; CURRENT APPLICATION NUMBER: US/10/641,834
; CURRENT FILING DATE: 2003-05-18
; PRIOR APPLICATION NUMBER: 09/639,667
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: linker peptide
US-10-641-834-3

Query Match      84.2%; Score 16; DB 16; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RVKR 4
DB      1 RVRR 4

US-10-399-127-29
; Sequence 29, Application US/10399127
; Publication No. US20040110690A1
; GENERAL INFORMATION:
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 NATL
; CURRENT APPLICATION NUMBER: US/10/399,127
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: PCT/IB01/02423
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-10-399-127-29

Query Match      84.2%; Score 16; DB 16; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RVKR 4
DB      1 RVRR 4

US-10-641-834-3
; Sequence 3, Application US/10641834
; Publication No. US20040209830A1
; GENERAL INFORMATION:
; APPLICANT: Russell, Stephen James
; APPLICANT: Peng, Kah Whye
; TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
; TITLE OF INVENTION: TRANSGENES
; FILE REFERENCE: 07039-292002
; CURRENT APPLICATION NUMBER: US/10/641,834
; CURRENT FILING DATE: 2003-05-18
; PRIOR APPLICATION NUMBER: 09/639,667
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: 60/149,168
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: linker peptide
US-10-641-834-3

Query Match      84.2%; Score 16; DB 16; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      1 RVKR 4
DB      1 RVRR 4
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Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
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Db 1 RLKR 4

RESULT 9

US-09-887-669-12
; Sequence 12, Application US/09887669
; Publication No. US20020082397A1
; GENERAL INFORMATION:
; APPLICANT: SCHLESSINGER, JOSEPH
; APPLICANT: SAP, JAN M.
; APPLICANT: ULLRICH, AXEL
; APPLICANT: VOGEL, WOLFGANG
; APPLICANT: FUCHS, MIRIAM
; TITLE OF INVENTION: NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-KAPPA
; FILE REFERENCE: 038602/1246
; CURRENT APPLICATION NUMBER: US/09/887,669
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: 09/234,883
; PRIOR FILING DATE: 1999-01-21
; PRIOR APPLICATION NUMBER: 08/087,244
; PRIOR FILING DATE: 1993-07-01
; PRIOR APPLICATION NUMBER: 08/049,384
; PRIOR FILING DATE: 1993-04-21
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: cleavage motif
US-09-887-669-12

Query Match 78.9%; Score 15; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 10

US-09-841-730-23
; Sequence 23, Application US/09841730
; Patent No. US20020157126A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/09/841,730
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Eukaryotes

; FEATURE:
; NAME/KEY: SITE
; LOCATION: (0)...(0)
; OTHER INFORMATION: proteolytic processing site
US-09-841-730-23

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Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RIRR 4

RESULT 11

US-09-997-868-22
; Sequence 22, Application US/09997868
; Publication No. US20030031654A1
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.,
; Groskreutz, Debyra J.
; TITLE OF INVENTION: Prohormone Convertase Transformed Cells and
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/997,868
; FILING DATE: 12-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/887265
; FILING DATE: 22-MAY-1992
; APPLICATION NUMBER: 07/803631
; FILING DATE: 06-DEC-1992
; APPLICATION NUMBER: PCT/US92/10621
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0748P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-997-868-22

Query Match 78.9%; Score 15; DB 10; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 12

US-10-013-032-23
; Sequence 23, Application US/10013032
; Publication No. US20020155544A1
; GENERAL INFORMATION:
; APPLICANT: Hullett, Debra A
; APPLICANT: Alam, Tausif
; APPLICANT: Sollinger, Hans W.
; TITLE OF INVENTION: Treatment of Diabetes with Synthetic Beta Cells
; FILE REFERENCE: 96429/9003CIP
; CURRENT APPLICATION NUMBER: US/10/013,032
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/537,696
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,888
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:amino acid
; OTHER INFORMATION: sequence of the B-C junction of mutant human
; OTHER INFORMATION: insulin
US-10-013-032-23

Query Match 78.9%; Score 15; DB 13; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
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Db 1 RTKR 4

RESULT 13
US-10-074-956-26
; Sequence 26, Application US/10074956
; Publication No. US2002019332A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
; FILE REFERENCE: 08191-022001
; CURRENT APPLICATION NUMBER: US/10/074,956
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/268,175
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Furin site
US-10-074-956-26

Query Match 78.9%; Score 15; DB 13; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.5e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
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Db 1 RIKR 4

RESULT 14
US-10-115-134-60
; Sequence 60, Application US/10115134
; Publication No. US2003022397A1
; GENERAL INFORMATION:
; APPLICANT: LEY, Arthur Charles

; APPLICANT: GUTERMAN, Sonia Kosow
; APPLICANT: MARKLAND, William
; APPLICANT: KENT, Rachel Baribault
; APPLICANT: ROBERTS, Bruce Lindsay
; APPLICANT: LADNER, Robert Charles
; TITLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS
; FILE REFERENCE: LEY-1C
; CURRENT APPLICATION NUMBER: US/10/115,134
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 08/849,406
; PRIOR FILING DATE: 2001-07-21
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: 39-42 of BRINK
US-10-115-134-60

Query Match 78.9%; Score 15; DB 15; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.5e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
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Db 1 RAKR 4

RESULT 15
US-10-831-302-15
; Sequence 15, Application US/10831302
; Publication No. US20050003482A1
; GENERAL INFORMATION:
; APPLICANT: Fang, Jianmin
; APPLICANT: Jooss, Karin
; APPLICANT: Qian, Jing-Jing
; TITLE OF INVENTION: Compositions and Methods for Enhanced Expression of
; TITLE OF INVENTION: Immunoglobulins From A Single Vector Using a Peptide
; TITLE OF INVENTION: Cleavage Site
; FILE REFERENCE: 3802-092-27CIP
; CURRENT APPLICATION NUMBER: US/10/831,302
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 10/452,253
; PRIOR FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: US 60/540,554
; PRIOR FILING DATE: 2004-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: furin cleavage site sequence
US-10-831-302-15

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Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 RAKR 4

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Job time : 106 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

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Searched: 6959266 seqs, 116806243 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

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SUMMARIES

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2	19	100.0	4	30	US-10-478-179-8	Sequence 8, Appli
3	16	84.2	4	1	PCT-US02-19394-69	Sequence 69, Appli
4	16	84.2	4	1	PCT-US03-05015-19	Sequence 19, Appli
5	16	84.2	4	7	US-08-398-028A-73	Sequence 73, Appli
6	16	84.2	4	8	US-08-460-343A-73	Sequence 73, Appli
7	16	84.2	4	9	US-08-504-265A-73	Sequence 73, Appli
8	16	84.2	4	17	US-09-372-003-4	Sequence 4, Appli
9	16	84.2	4	17	US-09-372-003-20	Sequence 20, Appli
10	16	84.2	4	19	US-09-566-922A-19	Sequence 19, Appli
11	16	84.2	4	19	US-09-566-922C-19	Sequence 19, Appli
12	16	84.2	4	25	US-09-977-831-29	Sequence 29, Appli
13	16	84.2	4	27	US-10-155-886-24	Sequence 24, Appli
14	16	84.2	4	27	US-10-165-015-29	Sequence 29, Appli
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24	15	78.9	4	3	US-07-887-265A-22	Sequence 22, Appli
25	15	78.9	4	6	US-08-200-900-36	Sequence 36, Appli
26	15	78.9	4	6	US-08-200-900-38	Sequence 38, Appli
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70 14 73.7 4 33 US-10-716-326-34 Sequence 34, Appl
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89 13 68.4 4 4 US-08-082-440-8 Sequence 8, Appl
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92 13 68.4 4 7 US-08-385-207-20 Sequence 20, Appl
93 13 68.4 4 7 US-08-385-209-20 Sequence 20, Appl
94 13 68.4 4 12 US-08-814-394A-9 Sequence 9, Appl
95 13 68.4 4 14 US-09-006-298-28 Sequence 28, Appl
96 13 68.4 4 14 US-09-011-006C-52 Sequence 52, Appl
97 13 68.4 4 14 US-09-049-770-4 Sequence 4, Appl
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100 13 68.4 4 16 US-09-287-145-56 Sequence 56, Appl

ALIGNMENTS

RESULT 1
US-09-885-914B-3
; Sequence 3, Application US/09885914B
; GENERAL INFORMATION:
; APPLICANT: DUBOIS, Claire
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; FILE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885, 914B
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213, 995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Arg at position 4 is modified at its carboxyl group with a -CH2CH
US-09-885-914B-3
Query Match 100.0%; Score 19; DB 23; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; APPLICANT: Board of Regents of the University of Nebraska
; GENERAL INFORMATION:
; TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
; FILE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
; FILE REFERENCE: 85761-28
; CURRENT APPLICATION NUMBER: US/09/885, 914B
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US 60/213, 995
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: CA 2,312,109
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (4)..(4)
; OTHER INFORMATION: Arg at position 4 is modified at its carboxyl group with a -CH2CH

Db 1 RVKR 4
RESULT 2
US-10-478-179-8
; Sequence 8, Application US/10478179
; GENERAL INFORMATION:
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: CHIMERIC ANTIGEN-SPECIFIC T
; TITLE OF INVENTION: CELL-ACTIVATING POLYPEPTIDES
; FILE REFERENCE: 07039-277US1
; CURRENT APPLICATION NUMBER: US/10/478,179
; CURRENT FILING DATE: 2003-11-18
; PRIOR APPLICATION NUMBER: PCT/US02/15992
; PRIOR FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US 60/291,874
; PRIOR FILING DATE: 2001-05-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: linker peptide
US-10-478-179-8

Query Match 100.0%; Score 19; DB 30; Length 4;
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 3
PCT-US02-19394-69
; Sequence 69, Application PC/TUS0219394
; GENERAL INFORMATION:
; APPLICANT: Komiya, Tomoko
; APPLICANT: Fuller, Robert S.
; TITLE OF INVENTION: Eglin C Based Drugs for Treatment of Disease
; FILE REFERENCE: UM-07240
; CURRENT APPLICATION NUMBER: PCT/US02/19394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/299,096
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
PCT-US02-19394-69

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
Db 1 RVKR 4

RESULT 4
PCT-US03-05015-19
; Sequence 19, Application PC/TUS0305015
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Nebraska

QY 1 RVKR 4

; APPLICANT: Sanderson, Sam D.G.
; APPLICANT: Vennerstrom, Jonathan L.
; APPLICANT: Thiele, Geoffrey M.
; APPLICANT: Parameswaran, Maniyan
; APPLICANT: Bevins, Rick A.
; APPLICANT: Srinivasa, Cheruku R.
; TITLE OF INVENTION: Compositions and compounds for use as a
; TITLE OF INVENTION: nicotine vaccine employing response selective agonist of an
; TITLE OF INVENTION: antigen-presenting cell receptor as a molecular adjuvant
; FILE REFERENCES: UNMCS744.1
; CURRENT APPLICATION NUMBER: PCT/US03/05015
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/360,967
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
PCT-US03-05015-19

Query Match 84.2%; Score 16; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

RESULT 5
US-08-398-028A-73
; Sequence 73, Application US/08398028A
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITIN VARIANTS CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,028A
FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-028A-73

Query Match 84.2%; Score 16; DB 7; Length 4;

Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

RESULT 6
US-08-460-343A-73
; Sequence 73, Application US/08460343A
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITIN VARIANTS CAPABLE OF CLEAVING
; TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,343A
FILING DATE: 01-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-mar-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-460-343A-73

Query Match 84.2%; Score 16; DB 8; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVR 4

RESULT 7
US-08-504-265A-73
; Sequence 73, Application US/08504265A
; GENERAL INFORMATION:
; APPLICANT: Marcus D. Ballinger and James A. Wells
; TITLE OF INVENTION: SUBSTITIN VARIANTS CAPABLE OF
; TITLE OF INVENTION: CLEAVING SUBSTRATES CONTAINING BASIC RESIDUES
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,265A
FILING DATE: 19-Jul-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936P1
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-504-265A-73

Query Match 84.2%; Score 16; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0;

QY 1 RVKR 4
|||
DB 1 RVRR 4

RESULT 8
US-09-372-003-4
Sequence 4, Application US/09372003
GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-372-003-4

Query Match 84.2%; Score 16; DB 17; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
DB 1 RVRR 4

RESULT 9
US-09-372-003-20
Sequence 20, Application US/09372003
GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified site
LOCATION: 1..4
OTHER INFORMATION: /label=Modified site
OTHER INFORMATION: /note="The amino terminus us derivatized by a
OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus

; OTHER INFORMATION: is derivatized by a 4-methylcoumaryl-7-amide group."
US-09-372-003-20

Query Match 84.2%; Score 16; DB 17; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVRR 4

RESULT 10

US-09-566-922A-19
; Sequence 19, Application US/09566922A
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Nebraska
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED
; FILE REFERENCE: UNMC5736
; CURRENT APPLICATION NUMBER: US/09/566,922A
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 09/051,685
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: PCT/US96/16825
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: US 60/005,727
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: synthetic sequence
US-09-566-922A-19

Query Match 84.2%; Score 16; DB 19; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVRR 4

RESULT 11

US-09-566-922C-19
; Sequence 19, Application US/09566922C
; GENERAL INFORMATION:
; APPLICANT: The Board of Regents of the University of Nebraska
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED
; FILE REFERENCE: UNMC5736
; CURRENT APPLICATION NUMBER: US/09/566,922C
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 09/051,685
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: PCT/US96/16825
; PRIOR FILING DATE: 1996-10-18
; PRIOR APPLICATION NUMBER: US 60/005,727
; PRIOR FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic sequence

US-09-566-922C-19

Query Match 84.2%; Score 16; DB 19; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVRR 4

RESULT 12

US-09-977-831-29
; Sequence 29, Application US/09977831
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: U.S.S.N. 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-09-977-831-29

Query Match 84.2%; Score 16; DB 25; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVRR 4

RESULT 13

US-10-155-886-24
; Sequence 24, Application US/10155886
; GENERAL INFORMATION:
; APPLICANT: Hempstead, Barbara L.
; APPLICANT: Lee, Ramee
; APPLICANT: Teng, Kenneth K.
; APPLICANT: Kermani, Pouneh
; TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
; FILE REFERENCE: 955-21 Sequence Nos. 1-68
; CURRENT APPLICATION NUMBER: US/10/155,886
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-155-886-24

Query Match 84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
||:|
Db 1 RVRR 4

RESULT 14

US-10-165-015-29
; Sequence 29, Application US/10165015
; GENERAL INFORMATION:
; APPLICANT: PACTI, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 CIP
; CURRENT APPLICATION NUMBER: US/10/165,015
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 09/977,831
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
; OTHER INFORMATION: PEPTIDE
US-10-165-015-29

Query Match 84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVRK 4

RESULT 15
US-10-173-524-69
; Sequence 69, Application US/10173524
; GENERAL INFORMATION:
; APPLICANT: Komiyama, Tomoko
; APPLICANT: Fuller, Robert S.
; TITLE OF INVENTION: Eglin C Based Drugs for Treatment of Disease
; FILE REFERENCE: UM-07240
; CURRENT APPLICATION NUMBER: US/10/173,524
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 60/299,096
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-173-524-69

Query Match 84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVRK 4

Search completed: June 20, 2005, 16:46:44
Job time : 330.5 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:30:17 ; Search time 37 Seconds
(without alignments)
13.327 Million cell updates/sec

Title: US-09-885-914B-3

Perfect score: 19

Sequence: 1 RVKR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 583429 seqs, 123271311 residues

Total number of hits satisfying chosen parameters: 4687

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Pending Patents AA New:*

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2: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*

3: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*

4: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*

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8: /cgn2_6/ptodata/2/paa/US13_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	84.2	4	6	US-10-892-402-110
2	15	78.9	4	5	US-09-997-868A-22
3	15	78.9	4	6	US-10-857-498A-11
4	15	78.9	4	7	US-11-051-267-23
5	15	78.9	4	7	US-11-127-629-23
6	14	73.7	4	7	US-11-129-741-2596
7	13	68.4	4	5	US-09-997-868A-23
8	13	68.4	4	6	US-10-892-402-107
9	13	68.4	4	6	US-10-892-402-108
10	13	68.4	4	6	US-10-892-402-109
11	13	68.4	4	6	US-10-386-418A-25
12	13	68.4	4	6	US-10-061-395B-43
13	13	68.4	4	7	US-11-004-794A-81
14	13	68.4	4	7	US-11-004-795A-97
15	13	68.4	4	7	US-11-107-481-17
16	13	68.4	4	7	US-11-004-399-1871
17	13	68.4	4	7	US-11-126-817-55
18	13	68.4	4	7	US-11-127-629-19
19	12	63.2	4	5	US-09-997-868A-24
20	12	63.2	4	6	US-10-892-402-122
21	12	63.2	4	7	US-11-065-669-23
22	12	63.2	4	7	US-11-080-973-23
23	12	63.2	4	7	US-11-106-718-21
24	12	63.2	4	7	US-11-129-741-2008
25	11	57.9	4	5	US-09-978-498-12

26	11	57.9	4	5	US-09-784-950A-106	Sequence 106, App
27	11	57.9	4	6	US-10-356-656-13	Sequence 13, Appl
28	11	57.9	4	6	US-10-892-402-12	Sequence 12, Appl
29	11	57.9	4	6	US-10-892-402-60	Sequence 60, Appl
30	11	57.9	4	6	US-10-892-402-102	Sequence 102, App
31	11	57.9	4	6	US-10-892-402-106	Sequence 106, App
32	11	57.9	4	6	US-10-892-402-146	Sequence 146, App
33	11	57.9	4	6	US-10-892-402-152	Sequence 152, App
34	11	57.9	4	6	US-10-684-796-380	Sequence 380, App
35	11	57.9	4	6	US-10-071-395-12	Sequence 12, Appl
36	11	57.9	4	7	US-11-004-399-3559	Sequence 3559, Ap
37	11	57.9	4	7	US-11-033-039-3	Sequence 3, Appli
38	11	57.9	4	7	US-11-033-039-8	Sequence 8, Appli
39	11	57.9	4	7	US-11-033-039-801	Sequence 801, App
40	10	52.6	3	1	PCT-US04-26288-109	Sequence 109, App
41	10	52.6	3	1	PCT-US04-26288-110	Sequence 110, App
42	10	52.6	3	1	PCT-US04-26288-119	Sequence 119, App
43	10	52.6	3	1	PCT-US04-26288-120	Sequence 120, App
44	10	52.6	3	1	PCT-US04-26288-134	Sequence 134, App
45	10	52.6	3	1	PCT-US04-26288-144	Sequence 144, App
46	10	52.6	3	1	PCT-US04-26288-145	Sequence 145, App
47	10	52.6	3	1	PCT-US04-26288-152	Sequence 152, App
48	10	52.6	3	1	PCT-US04-26288-153	Sequence 153, App
49	10	52.6	3	1	PCT-US04-26288-159	Sequence 159, App
50	10	52.6	3	1	PCT-US04-26288-160	Sequence 160, App
51	10	52.6	3	1	PCT-US04-26288-165	Sequence 165, App
52	10	52.6	3	1	PCT-US04-26288-169	Sequence 169, App
53	10	52.6	3	1	PCT-US05-11740-7	Sequence 7, Appli
54	10	52.6	3	6	US-10-472-963-801	Sequence 801, App
55	10	52.6	3	6	US-10-994-612-15	Sequence 15, Appl
56	10	52.6	3	6	US-10-994-612-19	Sequence 19, Appl
57	10	52.6	4	1	PCT-US05-04041-44	Sequence 44, Appl
58	10	52.6	4	1	PCT-US05-04041-45	Sequence 45, Appl
59	10	52.6	4	1	PCT-US05-02996-20	Sequence 20, Appl
60	10	52.6	4	1	PCT-US04-26288-238	Sequence 238, App
61	10	52.6	4	1	PCT-US04-26288-239	Sequence 239, App
62	10	52.6	4	1	PCT-US04-26288-258	Sequence 258, App
63	10	52.6	4	1	PCT-US04-26288-259	Sequence 259, App
64	10	52.6	4	1	PCT-US04-26288-273	Sequence 273, App
65	10	52.6	4	1	PCT-US04-26288-283	Sequence 283, App
66	10	52.6	4	1	PCT-US04-26288-284	Sequence 284, App
67	10	52.6	4	1	PCT-US04-26288-292	Sequence 292, App
68	10	52.6	4	1	PCT-US04-26288-293	Sequence 293, App
69	10	52.6	4	1	PCT-US04-26288-298	Sequence 298, App
70	10	52.6	4	1	PCT-US04-26288-299	Sequence 299, App
71	10	52.6	4	1	PCT-US04-26288-301	Sequence 301, App
72	10	52.6	4	1	PCT-US04-26288-302	Sequence 302, App
73	10	52.6	4	1	PCT-US04-26288-307	Sequence 307, App
74	10	52.6	4	1	PCT-US04-26288-308	Sequence 308, App
75	10	52.6	4	1	PCT-US04-26288-310	Sequence 310, App
76	10	52.6	4	1	PCT-US04-26288-311	Sequence 311, App
77	10	52.6	4	1	PCT-US04-26288-316	Sequence 316, App
78	10	52.6	4	1	PCT-US04-26288-317	Sequence 317, App
79	10	52.6	4	1	PCT-US04-26288-384	Sequence 384, App
80	10	52.6	4	1	PCT-US04-26288-386	Sequence 386, App
81	10	52.6	4	1	PCT-US04-26288-401	Sequence 401, App
82	10	52.6	4	1	PCT-US04-26288-409	Sequence 409, App
83	10	52.6	4	1	PCT-US04-26288-411	Sequence 411, App
84	10	52.6	4	1	PCT-US04-26288-414	Sequence 414, App
85	10	52.6	4	1	PCT-US04-26288-415	Sequence 415, App
86	10	52.6	4	1	PCT-US04-26288-416	Sequence 416, App
87	10	52.6	4	1	PCT-US04-26288-417	Sequence 417, App
88	10	52.6	4	1	PCT-US04-26288-419	Sequence 419, App
89	10	52.6	4	1	PCT-US04-26288-420	Sequence 420, App
90	10	52.6	4	1	PCT-US04-26288-421	Sequence 421, App
91	10	52.6	4	1	PCT-US04-26288-422	Sequence 422, App
92	10	52.6	4	1	PCT-US04-26288-424	Sequence 424, App
93	10	52.6	4	1	PCT-US04-26288-425	Sequence 425, App
94	10	52.6	4	1	PCT-US04-26288-426	Sequence 426, App
95	10	52.6	4	1	PCT-US04-26288-427	Sequence 427, App
96	10	52.6	4	1	PCT-US04-26288-428	Sequence 428, App
97	10	52.6	4	1	PCT-US04-26288-430	Sequence 430, App
98	10	52.6	4	1	PCT-US04-26288-431	Sequence 431, App

Sequence 432, App
Sequence 449, App

99 10 52.6 4 1 PCT-US04-26288-432
100 10 52.6 4 1 PCT-US04-26288-449

ALIGNMENTS

```
RESULT 1
US-10-892-402-110
; Sequence 110, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winesinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 110
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-110
```

Query Match 84.2%; Score 16; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RVRR 4

```
RESULT 2
US-09-997-868A-22
; Sequence 22, Application US/09997868A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.
; APPLICANT: Groskreutz, Debyra J.
; TITLE OF INVENTION: PROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE SYNTHESIS
; FILE REFERENCE: 11669.103USW3
; CURRENT APPLICATION NUMBER: US/09/997,868A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 08/026,143
; PRIOR FILING DATE: 1993-03-01
; PRIOR APPLICATION NUMBER: PCT/US92/10621
; PRIOR FILING DATE: 1992-12-04
; PRIOR APPLICATION NUMBER: US 07/887,265
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: US 07/803,631
; PRIOR FILING DATE: 1991-12-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-997-868A-22
```

Query Match 78.9%; Score 15; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RYKR 4

```
RESULT 3
US-10-857-498A-11
; Sequence 11, Application US/10857498A
; GENERAL INFORMATION:
; APPLICANT: Ko, Derek
; APPLICANT: Li, Yuanhao
; APPLICANT: Harding, Thomas
; APPLICANT: Fang, Jianmin
; APPLICANT: Ramesh, Nagarajan
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: Cell Specific Replication-Competent Viral Vectors Comprising
; TITLE OF INVENTION: a Self Processing Peptide Cleavage Site
; FILE REFERENCE: 3802-095-27
; CURRENT APPLICATION NUMBER: US/10/857,498A
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,005
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exemplary additional proteolytic cleavage site
US-10-857-498A-11
```

Query Match 78.9%; Score 15; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
DB 1 RAKR 4

```
RESULT 4
US-11-051-267-23
; Sequence 23, Application US/11051267
; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin
; APPLICANT: McPherron, Alexandra C.
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
; TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
; FILE REFERENCE: JHU1470-2
; CURRENT APPLICATION NUMBER: US/11/051,267
; CURRENT FILING DATE: 2005-02-03
; PRIOR APPLICATION NUMBER: US/09/841,730
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: 09/626,896
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/485,046
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: PCT/US98/15598
; PRIOR FILING DATE: 1998-07-28
; PRIOR APPLICATION NUMBER: 60/054,461
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Eukaryotes
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (0)...(0)
; OTHER INFORMATION: proteolytic processing site
```


US-11-051-267-23

Query Match 78.9%; Score 15; DB 7; Length 4;
Best Local Similarity 50.0%; Pred. No. 5.4e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RIRR 4

RESULT 5

US-11-127-629-23
; Sequence 23, Application US/11127629
; GENERAL INFORMATION:
; APPLICANT: Alam, Tausif
; APPLICANT: Hullett, Debra A.
; APPLICANT: Sollinger, Hans W.
; TITLE OF INVENTION: Treatment of Diabetes with Synthetic Beta Cells
; FILE REFERENCE: 960296.00216
; CURRENT APPLICATION NUMBER: US/11/127,629
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 10/923,924
; PRIOR FILING DATE: 2004-08-23
; PRIOR APPLICATION NUMBER: 10/013,032
; PRIOR FILING DATE: 2001-11-12
; PRIOR APPLICATION NUMBER: 09/537,696
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 09/115,888
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 08/786,625
; PRIOR FILING DATE: 1997-01-21
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: amino acid sequence of the B-C junction of mutant human insulin
US-11-127-629-23

Query Match 78.9%; Score 15; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RTKR 4

RESULT 6

US-11-129-741-2596
; Sequence 2596, Application US/11129741
; GENERAL INFORMATION:
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: WOO, CHIU YAT PATRICK
; APPLICANT: LAU, KAR PUI SUSANNA
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: PEIRIS, JOSEPH S.M.
; APPLICANT: GUAN, YI
; TITLE OF INVENTION: A NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
; TITLE OF INVENTION: INFECTION AND USES THEREOF
; FILE REFERENCE: V0690.0044
; CURRENT APPLICATION NUMBER: US/11/129,741
; CURRENT FILING DATE: 2005-05-16
; PRIOR APPLICATION NUMBER: 10/895,064
; PRIOR FILING DATE: 2004-07-21
; NUMBER OF SEQ ID NOS: 4257
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 2596
; LENGTH: 4

; TYPE: PRT
; ORGANISM: Corononavirius-HKU1
US-11-129-741-2596

Query Match 73.7%; Score 14; DB 7; Length 4;
Best Local Similarity 100.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RVK 3
|:|
Db 2 RVK 4

RESULT 7

US-09-997-868A-23
; Sequence 23, Application US/09997868A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Cornelia M.
; APPLICANT: Groskreutz, Debyra J.
; TITLE OF INVENTION: PROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE SYNTHESIS
; FILE REFERENCE: 11669.103USW3
; CURRENT APPLICATION NUMBER: US/09/997,868A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 08/026,143
; PRIOR FILING DATE: 1993-03-01
; PRIOR APPLICATION NUMBER: PCT/US92/10621
; PRIOR FILING DATE: 1992-12-04
; PRIOR APPLICATION NUMBER: US 07/887,265
; PRIOR FILING DATE: 1992-05-22
; PRIOR APPLICATION NUMBER: US 07/803,631
; PRIOR FILING DATE: 1991-12-06
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Peptide
US-09-997-868A-23

Query Match 68.4%; Score 13; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|:|
Db 1 RQKR 4

RESULT 8

US-10-892-402-107
; Sequence 107, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winsinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-107

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVTR 4

RESULT 9

US-10-892-402-108
; Sequence 108, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winessinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 108
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-108

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVPR 4

RESULT 10

US-10-892-402-109
; Sequence 109, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: Winessinger, Nicolas
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 021288-000410US
; CURRENT APPLICATION NUMBER: US/10/892,402
; CURRENT FILING DATE: 2004-07-14
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR FILING DATE: 2003-07-14
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 109
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-109

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RVDR 4

RESULT 11

US-10-386-414A-25
; Sequence 25, Application US/10386414A
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-0210WNIM
; CURRENT APPLICATION NUMBER: US/10/386,414A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/571,689
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cleavage Site
US-10-386-414A-25

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RVKR 4
|||
Db 1 RKKR 4

RESULT 12

US-10-061-395B-43
; Sequence 43, Application US/10061395B
; GENERAL INFORMATION:
; APPLICANT: Zauderer, Maurice

; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Identifying Regulator Molecules
; FILE REFERENCE: 1821.0080003
; CURRENT APPLICATION NUMBER: US/10/061,395B
; CURRENT FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/271,423
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/265,880
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/265,589
; PRIOR FILING DATE: 2001-02-02
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heterologous signal sequence for the nucleus
US-10-061-395B-43

Query Match 68.4%; Score 13; DB 6; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVKR 4
Db 1 RKKR 4

RESULT 13
US-11-004-794A-81
; Sequence 81, Application US/11004794A
; GENERAL INFORMATION:
; APPLICANT: Michael Kinch
; TITLE OF INVENTION: Targeted Drug Delivery Using EphA2 or
; FILE REFERENCE: 10271-120-999
; CURRENT APPLICATION NUMBER: US/11/004,794A
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: 60/527,396
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 125
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-794A-81

Query Match 68.4%; Score 13; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVKR 4
Db 1 RKKR 4

RESULT 14
US-11-004-795A-97
; Sequence 97, Application US/11004795A
; GENERAL INFORMATION:
; APPLICANT: Kinch, Michael
; TITLE OF INVENTION: EphA2, EphA4 and LMW-PTP and Methods of
; FILE REFERENCE: 10271-111-999
; CURRENT APPLICATION NUMBER: US/11/004,795A
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: 60/527,154
; PRIOR FILING DATE: 2003-12-04
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 97
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-795A-97
Query Match 68.4%; Score 13; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVKR 4
Db 1 RKKR 4
RESULT 15
US-11-107-481-17
; Sequence 17, Application US/11107481
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M.
; APPLICANT: Basler, Konard
; APPLICANT: Yamada, Toshiya
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1
; FILE REFERENCE: 0575/40314-A
; CURRENT APPLICATION NUMBER: US/11/107,481
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US/10/002,278
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Chick
US-11-107-481-17

Query Match 68.4%; Score 13; DB 7; Length 4;
Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 RVKR 4
Db 1 RSKR 4
Search completed: June 20, 2005, 16:48:02
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:37:50 ; Search time 41 Seconds
(without alignments)
924.620 Million cell updates/sec

Title: PDX1

Perfect score: 2032

Sequence: 1 EDQGDAAQKTDTSHHDDQH.....IEQNTKSPLEFMGVNPTGK 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

PIR 79:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	98.6	418	1 ITHU	alpha-1-antitrypsin
2	1870	92.0	409	1 ITBA	alpha-1-antitrypsin
3	1443.5	71.0	411	1 ITRT	alpha-1-antitrypsin
4	1431.5	70.4	413	2 S60036	alpha-1-antitrypsin
5	1430	70.4	416	1 ITSH	alpha-1-antitrypsin
6	1409	69.3	416	2 S21097	alpha-1-antitrypsin
7	1352	66.5	406	2 JX0346	alpha-1-antitrypsin
8	1335	65.7	413	2 S54981	alpha-1-antitrypsin
9	1327	65.3	413	2 I49470	alpha-1-antitrypsin
10	1322	65.1	413	2 JX0154	alpha-1-antitrypsin
11	1321	65.0	402	2 I49471	alpha-1-antitrypsin
12	1321	65.0	413	2 I49472	alpha-1-antitrypsin
13	1320	65.0	413	2 I49452	alpha-1-antitrypsin
14	1315	64.7	413	2 JX0267	alpha-1-antitrypsin
15	1310	64.5	413	2 I49473	alpha-1-antitrypsin
16	1298	63.9	413	2 A54968	alpha-1-antitrypsin
17	1296	63.8	413	2 I56481	alpha-1-antitrypsin
18	1294	63.7	413	2 I49474	alpha-1-antitrypsin
19	1281.5	63.1	412	1 ITWSC	alpha-1-antitrypsin
20	1280	63.0	405	2 C39088	alpha-1-antitrypsin
21	1235	60.8	410	2 C39088	alpha-1-antitrypsin
22	1181.5	58.1	388	2 B39088	alpha-1-antitrypsin
23	1153.5	56.8	410	2 A45457	alpha-1-antitrypsin
24	1125	55.4	420	2 A28882	alpha-1-antitrypsin
25	834	41.0	410	2 I50494	serine proteinase
26	829	40.8	406	2 A39339	protein C inhibitor
27	824	40.6	418	2 JX0129	contrapsin precursor
28	822	40.5	418	2 S23675	contrapsin-related
29	819	40.3	427	2 A49518	kallistatin precursor

30	816	40.2	433	1 ITHUC	alpha-1-antichymot
31	813.5	40.0	416	2 B29131	kallikrein-binding
32	811.5	39.9	405	2 A28321	corticosteroid-bin
33	806	39.7	406	2 I53281	corticosteroid-bin
34	804	39.6	383	2 A36117	corticosteroid-bin
35	803.5	39.5	418	2 JH0494	alpha-1-antichymot
36	802	39.5	403	2 S08102	serine proteinase
37	797	39.2	408	2 S11320	serine proteinase
38	793	39.0	417	2 S19724	kallikrein-binding
39	788	38.8	430	2 A49190	corticosteroid-bin
40	786.5	38.7	412	2 I46421	thyroxine-binding
41	781.5	38.5	415	2 A47224	thyroxine-binding
42	771.5	38.0	418	1 S31507	serine proteinase
43	771.5	38.0	418	2 A39567	thyroxine-binding
44	750	36.9	412	2 S31505	serine proteinase
45	727	35.8	372	2 I50492	alpha-1-antitrypsin
46	717.5	35.3	397	2 S33415	corticosteroid-bin
47	716.5	35.3	396	2 A40066	corticosteroid-bin
48	708.5	34.9	213	2 A25420	alpha-1-antitrypsin
49	697.5	34.3	369	2 JH0493	alpha-1-antichymot
50	689.5	33.9	436	2 A42440	estrogen-regulated
51	555	27.3	280	2 A29035	thyroid hormone-re
52	546.5	26.9	436	2 JC4841	regeneration assoc
53	529.5	26.1	390	2 I38201	squamous cell carc
54	525.5	25.9	390	2 I38202	leupin precursor -
55	508	25.0	397	2 I39184	bomabin - human
56	507.5	25.0	376	2 B59273	proteinase inhibit
57	505.5	24.9	478	2 A54248	heparin cofactor I
58	498.5	24.5	480	2 I46990	heparin cofactor I
59	498	24.5	252	2 S66289	alpha-1-antichymot
60	495.5	24.4	376	1 A48681	placental thrombin
61	492.5	24.2	479	1 S41066	heparin cofactor I
62	487.5	24.0	378	2 S38962	serpin - pig
63	487.5	24.0	416	2 S19896	plasmaogen activa
64	485	23.9	379	2 A42421	leukocyte elastase
65	482	23.7	415	2 S20047	plasmaogen activa
66	481.5	23.7	378	2 A57488	proteinase inhibit
67	481	23.7	415	2 A32853	plasmaogen activa
68	475.5	23.4	374	2 A59273	proteinase inhibit
69	475.5	23.4	386	1 OACH	ovalbumin (validat
70	468.5	23.1	499	1 A37924	heparin cofactor I
71	468	23.0	400	2 JC4265	plasmaogen activa
72	465	22.9	410	2 S70647	neuroserpin precu
73	459.5	22.6	200	2 D41752	alpha-1-antitrypsin
74	456	22.4	402	1 S06745	plasmaogen activa
75	452	22.2	391	2 JC7118	headpin serine pro
76	446.5	22.0	402	1 ITHUP1	plasmaogen activa
77	440.5	21.7	388	1 DYCH	ovalbumin-related
78	435.5	21.4	465	1 S28219	antithrombin III p
79	432	21.3	420	2 S19208	uteroferin-associ
80	430	21.2	383	2 S11433	ovalbumin - Japane
81	430	21.2	402	1 A35032	plasmaogen activa
82	429.5	21.1	429	2 A33309	uterine milk prote
83	428.5	21.1	464	1 XHUH3	antithrombin III p
84	428	21.0	379	2 S27383	elastase inhibitor
85	427.5	21.0	433	1 A61435	antithrombin III -
86	426	21.0	405	1 A41252	heat shock protein
87	424	20.9	465	2 I59611	antithrombin III -
88	423	20.8	213	2 A26423	serine proteinase
89	422.5	20.8	402	1 A34761	plasmaogen activa
90	422	20.8	418	2 A53120	intracellular coag
91	420	20.7	374	2 AH1903	hypothetical prote
92	420	20.7	418	2 A47281	pigment epithelial
93	414.5	20.4	431	1 JX0364	antithrombin III -
94	411	20.2	418	2 I52968	colligin-2 - human
95	410	20.2	359	2 D88940	protein C05E4.1 [i
96	406	20.0	359	2 A46046	serine proteinase
97	401.5	19.8	417	1 A40968	heat shock protein
98	401.5	19.8	417	2 A34722	uteroferin-associ
99	400.5	19.7	417	1 A42843	heat shock protein
100	399.5	19.7	417	1 S20608	heat shock protein

ALIGNMENTS

RESULT 1

ITRU

alpha-1-antitrypsin precursor [validated] - human
 N:Alternate names: alpha-1-AT; alpha-1-proteinase inhibitor
 C:Species: Homo sapiens (nan)
 C>Date: 30-Nov-1980 #sequence_revision 31-Mar-1992 #ext_change 09-Jul-2004
 C:Accession: A21853; B21853; A93352; A90944; A58528; A23174; A93281; A32336; S14476; A24
 R:Long, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K.
 Biochemistry 23, 4828-4837, 1984
 A:Title: Complete sequence of the cDNA for human alpha-1-antitrypsin and the gene for th
 A:Reference number: A21853; MUID:85047150; PMID:6093867
 A:Accession: A21853
 A:Molecule type: mRNA
 A:Residues: 1-287,'V',289-418 <LON2>
 A:Cross-references: GB:K02212; NID:G177830; PIDN:AAB59495.1; PID:G177831
 A:Experimental source: M (normal) allele
 A:Accession: B21853
 A:Molecule type: DNA
 A:Residues: 1-287,'V',289-418 <LON2>
 A:Cross-references: GB:K02212; NID:G177830; PIDN:AAB59495.1; PID:G177831
 A:Experimental source: S variant allele
 R:Rosenberg, S.; Barr, P.J.; Najarian, R.C.; Hallowell, R.A.
 Nature 312, 77-80, 1984
 A:Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-1-
 A:Reference number: A93352; MUID:85036645; PMID:6387509
 A:Accession: A93352
 A:Molecule type: mRNA
 A:Residues: 1-124,'H',126-325,'I',327-418 <ROS>
 A:Cross-references: EMBL:X01683; NID:G28965
 R:Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; Lo
 DNA 2, 255-264, 1983
 A:Title: Cloning and expression in Escherichia coli of full-length complementary DNA cod
 A:Reference number: A90944; MUID:84107980; PMID:6319097
 A:Accession: A90944
 A:Molecule type: mRNA
 A:Residues: 1-138,'DG',141-272,'N',274-418 <BOI>
 A:Cross-references: GB:K01396; NID:G28965
 A:Note: this sequence has been corrected in reference A58528
 R:Colau, B.; Chuchana, P.; Bollen, A.
 DNA 3, 327-330, 1984
 A:Title: Revised sequence of full-length complementary DNA coding for human alpha-1-anti
 A:Reference number: A58528; MUID:85026667; PMID:6333329
 A:Contents: corrections to sequence in A90944
 A:Accession: A58528
 A:Molecule type: mRNA
 A:Residues: 1-418 <COL>
 A:Cross-references: GB:K01396; NID:G28965; PIDN:CAA25838.1; PID:G28966
 R:Ciliberto, G.; Dente, L.; Cortese, R.
 Cell 41, 531-540, 1985
 A:Title: Cell-specific expression of a transfected human alpha-1-antitrypsin gene.
 A:Reference number: A23174; MUID:85176977; PMID:2985281
 A:Accession: A23174
 A:Molecule type: mRNA
 A:Residues: 1-11,13-173,'H',175-228,'D',230-418 <CIL>
 A:Cross-references: GB:M11465; NID:G177826; PIDN:AA51546.1; PID:G177827
 A:Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var
 R:Carrell, R.W.; Jeppsson, J.O.; Laurelli, C.B.; Brennan, S.O.; Owen, M.C.; Vaughan, L.;
 Nature 298, 329-334, 1982
 A:Title: Structure and variation of human alpha-1-antitrypsin.
 A:Reference number: A93281; MUID:82220135; PMID:7045697
 A:Accession: A93281
 A:Molecule type: protein
 A:Residues: 25-418 <CAR>
 A:Note: peptide sequence differences with A21853 (Leu-200 and the amidation states of re
 R:Zhu, X.J.; Kang, S.S.; Hargrove, K.; Shochat, D.; Jarrells, M.; Mojesky, M.; Chan, S.K.
 Biochem. J. 246, 25-36, 1987
 A:Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor.
 A:Reference number: A32336; MUID:88049621; PMID:2445337
 A:Accession: A32336
 A:Molecule type: protein

A:Residues: 25-418 <ZHU>
 A:Note: peptides were sequenced or partially sequenced and ordered by comparison with A21
 R:Weiland, K.L.; Falany, C.N.; Dooley, T.P.
 submitted to the EMBL Data Library, December 1989
 A:Description: Identification of a cDNA encoding a variant form of the human proteolytic
 A:Reference number: S14476
 A:Accession: S14476
 A:Molecule type: mRNA
 A:Residues: 142-230,'V',232-338 <WEI>
 A:Cross-references: EMBL:X17122; NID:G28636; PIDN:CAA34982.1; PID:G28637
 A:Experimental source: a variant form
 R:Riley, J.H.; Bathurst, I.C.; Edbrooke, M.R.; Carrell, R.W.; Craig, R.K.
 FEBS Lett. 189, 361-366, 1985
 A:Title: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, acute phase
 A:Reference number: A24013; MUID:86005469; PMID:3876243
 A:Accession: A24013
 A:Molecule type: mRNA
 A:Residues: 292-418 <RIL>
 A:Cross-references: EMBL:X02920; NID:G24437; PIDN:CAA26677.1; PID:G24438
 R:Schulze, A.J.; Baumann, U.; Koef, S.; Jaeger, E.; Huber, R.; Laurelli, C.B.
 Eur. J. Biochem. 194, 51-56, 1990
 A:Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar
 A:Reference number: S13833; MUID:91071209; PMID:2253623
 A:Accession: S13833
 A:Molecule type: protein
 A:Residues: 25-41 <SCH>
 R:Niemann, M.A.; Narkates, A.J.; Miller, E.J.
 Matrix 12, 233-241, 1992
 A:Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal
 A:Reference number: S23516; MUID:93024095; PMID:1406456
 A:Accession: S23516
 A:Molecule type: protein
 A:Residues: 375-409,'L',411-413,'S' <NIE>
 R:Dengler, R.; Eger, G.; Lottspeich, F.; Plewan, A.; Ogilvie, A.; Emmerich, B.
 Biol. Chem. Hoppe-Seyler 373, 581-588, 1992
 A:Title: Proteolytic inactivation of alpha(1)-proteinase inhibitor in vivo: detection, c
 A:Reference number: S23962; MUID:92384968; PMID:1515087
 A:Accession: S23962
 A:Molecule type: protein
 A:Residues: 44-53;384-392 <DEN>
 R:Dengler, R.; Lottspeich, F.; Oberthuer, W.; Mast, A.E.; Emmerich, B.
 Biol. Chem. Hoppe-Seyler 376, 165-172, 1995
 A:Title: Limited proteolysis of alpha(1)-proteinase inhibitor (alpha(1)-PI) in acute leu
 A:Reference number: S55249; MUID:95336645; PMID:7612193
 A:Accession: S55249
 A:Molecule type: protein
 A:Residues: 25-28;43-47;207-208;382-389;414-418 <DE2>
 R:Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
 Nature 297, 655-659, 1982
 A:Title: Sequence homology and structural comparison between the chromosomal human alpha
 A:Reference number: I39371; MUID:82220035; PMID:6979715
 A:Accession: I39371
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-67 <LEI1>
 A:Cross-references: GB:J00064; NID:G177817; PIDN:AAB59369.1; PID:G177822
 A:Accession: I39172
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 196-225 <LSI2>
 A:Cross-references: GB:J00066; NID:G177819; PIDN:AAB59370.1; PID:G177823
 R:Chang, W.S.W.; Wardell, M.R.; Lomas, D.A.; Carrell, R.W.
 Biochem. J. 314, 647-653, 1996
 A:Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
 A:Reference number: S63599; MUID:96239126; PMID:8670081
 A:Accession: S63599
 A:Molecule type: protein
 A:Residues: 371-385 <CHA>
 R:Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamson, R.
 Biomed. Blochim. Acta 44, 421-431, 1985
 A:Title: Construction and partial characterization of a human liver cDNA library.
 A:Reference number: I39370; MUID:85225507; PMID:3873938
 A:Accession: I39370

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 387-399, 'D', 401-418 <COU>
A;Cross-references: GB:M26123; NID:G177815; PIDN:AAA51545.1; PID:G177816
R;Faber, J.P.; Weidinger, S.; Olek, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A;Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zausburg.
A;Reference number: A35338; MUID:90252805; PMID:2339709
A;Accession: A35338
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 122-124, 'H', 126-128, 363-365, 'K', 367-369 <FAB>
A;Experimental source: mutant PI Zausberg
A;Note: this Z mutation with Lys-366 arose from the M2 variant with His-125
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50775; PDB:7API
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 1, residues 4
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
submitted to the Brookhaven Protein Data Bank, September 1988
A;Reference number: A50810; PDB:9API
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 2, residues 4
R;Loebermann, H.; Tokuko, R.; Deisenhofer, J.; Huber, R.
J. Mol. Biol. 177, 531-556, 1984
A;Title: Human alpha-1-proteinase inhibitor. Crystal structure analysis of two crystal m
A;Reference number: A58525; MUID:84292309; PMID:6332197
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
R;Carrell, R.W.; Jeppsson, J.O.; Vaughan, L.; Brennan, S.O.; Owen, M.C.; Boswell, D.R.
FEBS Lett. 135, 301-303, 1981
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Reference number: A58526; MUID:82095611; PMID:6976274
A;Contents: annotation; carbohydrate attachment sites
C;Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indivi
sis.
C;Genetics:
A;Gene: GDB:PI
A;Cross-references: GDB:120289; OMIM:107400
A;Map position: 14q32.1-14q32.1
A;Introns: 216/1; 306/2; 355/3
A;Note: the first intron occurs before the initiator codon
C;Function:
A;Description: inhibitor of serine proteinases, primarily leukocyte elastase and collage
A;Note: it also inhibits plasmin, thrombin, kallikrein, trypsin, and chymotrypsin
C;Superfamily: Serpin
C;Keywords: acute phase; emphysema; glycoprotein; plasma; polymorphism; serine proteinase
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-418/Product: alpha-1-antitrypsin #status experimental <MAT>
F;70,107,271/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;382/Inhibitory site: Met (elastase, collagenase) #status experimental
Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-131;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGTADTHDEILGLNFNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTGNGFL 120
DB 85 FAMLSTGTADTHDEILGLNFNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTGNGFL 144
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNIYIFPKGWERPFVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 240
DB 205 VFALVNIYIFPKGWERPFVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 264

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 324
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTGAAGAMFLERIPSI 360
DB 325 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTGAAGAMFLERIPSI 384
QY 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPCTK 394
DB 385 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPCTK 418
RESULT 2
ITBA
N;Alternate names: alpha-1-proteinase precursor - baboon (fragment)
C;Species: Papio sp. (baboon)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 15-Sep-2003
C;Accession: A01248
R;Kurachi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Day
proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A;Title: Cloning and sequence of cDNA coding for alpha-1-antitrypsin.
A;Reference number: A01248; MUID:82082539; PMID:7031661
A;Accession: A01248
A;Molecule type: mRNA
A;Residues: 1-409 <KUR>
A;Cross-references: GB:J00321; NID:G176561; PIDN:AAA35377.1; PID:G176562
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target
psin.
C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-409/Product: alpha-1-antitrypsin #status predicted <MAT>
F;61,98,262/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;373/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match 92.0%; Score 1870; DB 1; Length 409;
Best Local Similarity 91.1%; Pred. No. 4.4e-122;
Matches 359; Conservative 21; Mismatches 14; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 60
DB 16 EDPOGDAAKTDTSHDQDHPFNKLTNPALAEFAPSLYQLAHQSNSTNIFPSPVSIATA 75
QY 61 FAMLSTGTADTHDEILGLNFNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTGNGFL 120
DB 76 FAMLSTGTADTHDEILGLNFNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTLTGNGFL 135
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 136 NKSLLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 195
QY 181 VFALVNIYIFPKGWERPFVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 240
DB 196 VFALVNIYIFPKGWERPFVKDTEEDFHVDDQVTTVKVPMKRLGMFNIOHCKKLSWVL 255
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 300
DB 256 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTVDLK 315
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTGAAGAMFLERIPSI 360
DB 316 TVLGHGIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTGAAGAMFLERIPSI 375
QY 361 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPCTK 394
DB 376 PPEVKFNKPFVFLMIQNTKSPFLFMGKVVNPCTK 409

RESULT 3
ITRT

alpha-1-antitrypsin precursor - rat
N:Alternate names: alpha-1-proteinase inhibitor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 31-Mar-1992 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: A33892; B33892; S08016; JX0123; A38823
R:Chao, S.; Chai, K.X.; Chao, L.; Chao, J.
Biochemistry 29, 323-329, 1990
A:Title: Molecular cloning and primary structure of rat alpha-1-antitrypsin.
A:Reference number: A33892; MUID:90148955; PMID:2302382
A:Accession: A33892
A:Molecule type: mRNA
A:Residues: 4-411 <CHA>
A:Cross-references: UNIPROT:P17475; GB:M32247; NID:G203062; PIDN:AAA40788.1; PID:G203063
A:Accession: B33892
A:Molecule type: protein
A:Residues: 25-57 <CH2>
R:Flink, I.L.; Bailey, T.; Morkin, E.
submitted to the EMBL Data Library, August 1989
A:Reference number: S08016
A:Accession: S08016
A:Molecule type: mRNA
A:Residues: 188-246; 'I', 248-321, 'D', 323-389 <FLI>
A:Cross-references: EMBL:X16273; NID:G57299; PIDN:CAA34349.1; PID:G930263
R:Misumi, Y.; Sohda, M.; Ohkubo, K.; Takami, N.; Oda, K.; Ikehara, Y.
J. Biochem. 108, 230-234, 1990
A:Title: Molecular cloning and sequencing of the cDNA of rat alpha-1-protease inhibitor
A:Reference number: JX0123; MUID:91035351; PMID:2229024
A:Accession: JX0123
A:Molecule type: mRNA
A:Residues: 1-13, 'G', 15-83, 'V', 85-247, 'Y', 249-317, 'N', 319-411 <MIS>
A:Cross-references: GB:D00675; NID:G220648; PIDN:BAA00579.1; PID:G220649
A:Experimental source: serum
A:Accession: A38823
A:Molecule type: protein
A:Residues: 25-45 <MI2>
C:Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary target is psl.
C:Superfamily: Serpin
C:Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-411/Product: alpha-1-antitrypsin #status experimental <MAT>
F;64,101,265/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;376/Inhibitory site: Met (elastase, collagenase) #status predicted
Query Match 71.0%; Score 1443.5; DB 1; Length 411;
Best Local Similarity 69.8%; Pred. No. 1.6e-92; Indels 1; Gaps 1;
Matches 269; Conservative 62; Mismatches 53;
QY 8 AOKTDTSHDQDHPFNKTPNLAEPFSLYRQLAHQSNSTNIFSPSVSIATAFAMLSLG 67
DB 27 AQETDTSQDDQS-PTVRKISSNLADFAFSLYRELHVQSNSTNIFSPSMITATAFAMLSLG 85
QY 68 TKADTHDEILEGNFNLTQIPEAQIHGFOELLRTLNQPSQLQLTGNGLFLSOGKLKLV 127
DB 86 SKGDRKQILEGLEFNLQIPEADHKAHFHLIQTLLNRDSELSQLNTGNGLFVNKNLKV 145
QY 128 DKFLEVDVKLYHSEAFVNFQGTQAKQINDYVEKGTQKIVDLVKELDRDTVFALVNY 187
DB 146 EXPLEEVKNYHSEAFVNFADSEAKKVINDYVEKGTQKIVDLVKELDRDTVFALVNY 205
QY 188 IPFKGWERPFVKDTEEDDFHVDQVTTVKVPMKRLGMFNIQHKCKLSSVLLMKYLG 247
DB 206 IPFKGKWKPFNFPEHTRDADFVDDKSTTVKVPMMRLGMFDMHYCSTLSSVLLMDYLG 265
QY 248 ATAIFLPEGKLOHLENLTHDIITKFLNEDRRASLHPLKSLTGTVDLKSVLGQLG 307
DB 266 ATAIFLLPDGKQKHLEQTLTKDLSRFLNRTSAILYFPKLSISGTYNLTKLLSSLG 325
QY 308 ITKVFENGLDLSGVTESEAPLKSVAHVKAVALTIDEGTEAAGAMFLERIPRSIPPEVKFN 367
DB 326 ITRVFENNDALSGITEDAPLKSQAHVKAVALTIDERGTEAAGATVVEAVPMSPPOVKFD 385
QY 368 KPFVFLMI EQNTKSPFLFMGKVVNPT 392

DB 386 HPFIFMIVESETQSPFLFVGKVIDPT 410
RESULT 4
S60036
alpha-1-antitrypsin precursor - golden hamster
N:Alternate names: alpha-1-antiproteinase
C:Species: Mesocricetus auratus (golden hamster)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
A:Accession: S60036
R:Nakatani, T.; Suzuki, Y.; Yoshida, K.; Sinohara, H.
Biochim. Biophys. Acta 1263, 245-248, 1995
A:Title: Molecular cloning and sequence analysis of cDNA encoding plasma alpha-1-antiprot
A:Reference number: S60036; MUID:96004896; PMID:7548212
A:Accession: S60036
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-413 <NAK>
A:Cross-references: UNIPROT:P97277; EMBL:D49709; NID:G1088432; PIDN:BAA08557.1; PID:G1794
A:Note: the source is designated as Syrian hamster
C:Superfamily: Serpin
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antitrypsin #status predicted <MAT>
Query Match 70.4%; Score 1431.5; DB 2; Length 413;
Best Local Similarity 70.2%; Pred. No. 1.1e-91;
Matches 271; Conservative 55; Mismatches 59; Indels 1; Gaps 1;
QY 8 AOKTDTSHDQDHPFNKTPNLAEPFSLYRQLAHQSNSTNIFSPSVSIATAFAMLSLG 67
DB 27 AQETDASKQDQEHQACCKIAPNLADFPFSLYRELHVQSNSTNIFSPSVSIATAFAMLSLG 86
QY 68 TKADTHDEILEGNFNLTQIPEAQIHGFOELLRTLNQPSQLQLTGNGLFLSOGKLKLV 127
DB 87 TKGVTHTQILEGLGNLTIAEAEVHKGFHNLQTFNRPDNLQLTGNGLFHNNKLKV 146
QY 128 DKFLEVDVKLYHSEAFVNFQGTQAKQINDYVEKGTQKIVDLVKELDRDTVFALVNY 187
DB 147 DFLFEEVKNYHSEAFVNFQGTQAKQINDYVEKGTQKIVDLVKELDRDTVFALVNY 206
QY 188 IPFKGWERPFVKDTEEDDFHVDQVTTVKVPMKRLGMFNIQHKCKLSSVLLMKYLG 247
DB 207 IPFKGKWKPFNFADNTEADDFHVDKTTTVKVPMSRLGMFDFVHYVSTLSSVLLMDYLG 266
QY 248 ATAIFLPEGKLOHLENLTHDIITKFLNEDRRASLHPLKSLTGTVDLKSVLGQLG 307
DB 267 ATAIFLLPDGKQKHLEQTLTKDLSRFLNRTSAILYFPKLSISGTYNLTKLLDPLG 326
QY 308 ITKVFENGLDLSGVTESEAPLKSVAHVKAVALTIDEGTEAAGAMFLERIPRSIPPEVKFN 367
DB 327 ITQVFSNGADLSGITEDVFLKGVKAVALTIDERGTEAAGATFWEIIPMSVPPPEVFN 386
QY 368 KPFVFLMI EQNT- KSPFLFMGKVVNPT 392
DB 387 SPFIALLYDRQAKSPFLFVGKVVDP 412
RESULT 5
ITSH
alpha-1-antitrypsin precursor - sheep
N:Alternate names: alpha-1-proteinase inhibitor
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
A:Accession: S05312
R:Brown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.; Wu, Y.
Nucleic Acids Res. 17, 6398, 1989
A:Title: Nucleotide and deduced amino acid sequence of sheep alpha-1 antitrypsin.
A:Reference number: S05312; MUID:89366677; PMID:2788872
A:Accession: S05312
A:Molecule type: mRNA
A:Residues: 1-416 <BRO>
A:Cross-references: UNIPROT:P12725; EMBL:X15555; NID:G1369; PIDN:CAA33561.1; PID:G1370

A;Note: the authors translated the codon ATC for residue 395 as Ala
C;Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its primary targeted psin.

C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-416/Product: alpha-1-antitrypsin #status predicted <MAT>
F;58,105,269/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;380/Inhibitory site: Met (elastase, collagenase) #status predicted

Query Match 70.4%; Score 1430; DB 1; Length 416;
Best Local Similarity 69.2%; Pred. No. 1.4e-91;
Matches 269; Conservative 62; Mismatches 56; Indels 2; Gaps 1;

QY 4 QGDAQAQKTDTHSHDQHPFTNKITPNLAFAPSLYRQLAQHSNSTNIFPSPVSIATAFAM 63
DB 28 QGHAVQETDDTAHQE--AACHKIAPNLANFAPSIYHKLAAHQSNSTNIFPSPVSIASAFAM 85
QY 64 LSLGTYADTHDEILGELNPNLTQIPEAQIHGFEQBLRLTNQPDQSOLQLTGNGLFLSQ 123
DB 86 LSLGAKGNTHTEILGELGNLTLEABEAIHKGFQHLHTLNQPNHQLTNGNGLFINES 145
QY 124 LKLVDFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 183
DB 146 AKLVDTFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 205
QY 184 LKLVDFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 243
DB 146 AKLVDTFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 205
QY 244 YLGNATAIFLPDEGKLOHLENLTHDIITKFLNEDRDSASLHLPKLSITGTIDLSKVL 303
DB 266 YVGNVTACFTLPDLGKLOQLLEKLNELLAKFLEKKYASSANLHLPKLSITSETYDLKTVL 325
QY 304 GOLGITYKVSNGADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGMFLERIPRISIPPE 363
DB 326 GEIGINRVFSNGADLSGITEQPLKVSALHKAALTIDKGTAAAGMFLERIPRISIPPE 385
QY 364 VKFNKPFVFLMIQNTKSPFLFMGKVVNPT 392
DB 386 VEFNRPFLCILYDRNTKSPFLFMGKVVNPT 414

RESULT 6
alpha-1-antitrypsin precursor - bovine
N;Alternate names: alpha-1-proteinase inhibitor; proteinase inhibitor Inh3
C;Species: Bos primigenius taurus (cattle)
C;Date: 07-Apr-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: S21097; PC2040; S18920
R;Sinha, D.; Bakshi, M.R.; Kirby, E.P.
Biochim. Biophys. Acta 1130, 209-212, 1992
A;Title: Complete cDNA sequence of bovine alpha-1-antitrypsin.
A;Reference number: S21097; MUID:922230396; PMID:1562597
A;Accession: S21097
A;Molecule type: mRNA
A;Residues: 1-416 <SIN>
A;Cross-references: UNIPROT:P34955; EMBL:X63129; NID:g41; PIDN:CAA44840.1; PID:g42
A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 209-TH
R;Sinha, D.; Yang, X.; Emig, F.; Kirby, E.P.
J. Biochem. 115, 387-391, 1994
A;Title: Isolation and characterization of two protease inhibitors from bovine plasma.
A;Reference number: PX0072; MUID:94334275; PMID:8056747
A;Accession: PC2040
A;Molecule type: protein
A;Residues: 25-44 <S2>
C;Superfamily: Serpin
C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-416/Product: alpha-1-antitrypsin #status predicted <MAT>
F;58,105,143,269/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 69.3%; Score 1409; DB 2; Length 416;

Best Local Similarity 68.4%; Pred. No. 4e-90;
Matches 266; Conservative 61; Mismatches 60; Indels 2; Gaps 1;

QY 4 QGDAQAQKTDTHSHDQHPFTNKITPNLAFAPSLYRQLAQHSNSTNIFPSPVSIATAFAM 63
DB 28 QGHAVQETDDTAHQE--AACHKIAPNLANFAPSIYHKLAAHQSNSTNIFPSPVSIASAFAM 85
QY 64 LSLGTYADTHDEILGELNPNLTQIPEAQIHGFEQBLRLTNQPDQSOLQLTGNGLFLSQ 123
DB 86 LSLGAKGNTHTEILGELGNLTLEABEAIHKGFQHLHTLNQPNHQLTNGNGLFINES 145
QY 124 LKLVDFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 183
DB 146 AKLVDTFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 205
QY 184 LKLVDFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFA 243
DB 206 LNYISFKGKWEKPEFVEHTERDFHVDQVTVKVPMMRLGMFNIOHCKKLSWVLLMK 265
QY 244 YLGNATAIFLPDEGKLOHLENLTHDIITKFLNEDRDSASLHLPKLSITGTIDLSKVL 303
DB 266 YVGNVTACFTLPDLGKLOQLLEKLNELLAKFLEKKYASSANLHLPKLSITSETYDLKTVL 325
QY 304 GOLGITYKVSNGADLSGVTEAPLKLKSAVHKAVLTIDKGTAAAGMFLERIPRISIPPE 363
DB 326 GVGITEVFSNGADLSGITEQPLKVSALHKAALTIDKGTAAAGMFLERIPRISIPPE 385
QY 364 VKFNKPFVFLMIQNTKSPFLFMGKVVNPT 392
DB 386 VEFNRPFLCILYDRNTKSPFLFMGKVVNPT 414

RESULT 7
alpha-1-antitrypsin precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0346; PC2357
J;Goto, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Sinohara, H.
J. Biochem. 116, 582-588, 1994
A;Title: Plasma alpha-1-antitrypsinase from the Mongolian gerbil, Meriones unguiculatus.
A;Reference number: JX0346; MUID:95155268; PMID:7852275
A;Accession: JX0346
A;Molecule type: mRNA
A;Residues: 1-406 <GOT>
A;Cross-references: UNIPROT:Q64118; GB:S77822; NID:G998663; PIDN:AAB33367.1; PID:G998664
A;Accession: PC2357
A;Molecule type: protein
A;Residues: 25-44; 77-96 <GOT>
A;Experimental source: plasma
C;Superfamily: Serpin
C;Keywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-406/Product: alpha-1-antitrypsinase #status predicted <MAT>
F;383-387/Region: serpin binding #status predicted
F;59,96,134,260,403/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;371/Inhibitory site: Met (trypsin, chymotrypsin, elastase) #status predicted

Query Match 66.5%; Score 1352; DB 2; Length 406;
Best Local Similarity 67.5%; Pred. No. 3.4e-86;
Matches 260; Conservative 58; Mismatches 61; Indels 6; Gaps 2;

QY 8 AOKTDTSHDQHPFTNKITPNLAFAPSLYRQLAQHSNSTNIFPSPVSIATAFAMLSUG 67
DB 27 AKETDSSH--QDH-----INASNLADFAFLYRVLHSHQSNSTNIFLPSLATAMLSUG 80
QY 68 TKADTHDEILGELNPNLTQIPEAQIHGFEQBLRLTNQPDQSOLQLTGNGLFLSQGLKLV 127
DB 81 SKDDTKAQLQLGLHFNLTETSEADIHKGQHLKTLNRPDNEQLTGTGSSFLVNNSLNV 140
QY 128 DKFLEDDVKLVHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFAVNV 187
DB 141 EKFLFEVKNHYHSEAFNFTGTEQAKKQINDYVEKGTGQKIVDLVKELDRDTVFAVNV 200

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QY 188 IFKQKWERPEVKDTEEDFHVDQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYLG 247
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 201 IFRGKWEKFPDELFEADFDYDKSTTVKVPMMNRGMGFVHYCDTLSSWVLLMDYLG 260

QY 248 ATAIFLPDQKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTVDKLSVLGQLG 307
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 261 ATAIFLPDQKQOHLQETLTKSHIYKFLQNRHTRGSANVHLPKLSISGTYNLKVLSPLG 320

QY 308 ITKVFNSGADLSGVTEAPLKSVAHVKAULTTDEKTEAAGAMFLERIPRSIPPEVKFN 367
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 321 ITQVFNAGDLSGITTDVPLKLSVAHVKAULTLDERGTEAAGTVVLEAVPMSIPPDVCFK 380

QY 368 KPVFLMIEQNTKSPFLFMGVNPT 392
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 381 NPFVVICDKHTQSPFLFVGKVNPT 405

RESULT 8
S54981
alpha-1-antiprotease isoform E precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 28-Oct-1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
R:Accession: S54981; S72199
R:Saito, A.; Sinohara, H.
Biochem. J. 307, 369-375, 1995
A:Title: Rabbit alpha-1-antiprotease E: a novel recombinant serpin which does not inhibit
A:Reference number: S54981; MUID:95251597; PMID:7733871
A:Accession: S54981
A:Molecule type: mRNA
A:Residues: 1-413 <SA11>
A:Cross-references: UNIPROT:Q28665; EMBL:D17725; NID:g1008927; PIDN:BAA04579.1; PID:g100
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antiprotease E #status experimental <MAT>

Query Match 65.7%; Score 1335; DB 2; Length 413;
Best Local Similarity 65.1%; Pred. No. 5.3e-85;
Matches 252; Conservative 60; Mismatches 75; Indels 0; Gaps 0;

QY 6 DAAQKTDTSDDHPTFNKIPNLAEPAFSLYROLAHOQSNSTNIFFSPVSIATAFAMLS 65
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 25 DEAQETAVSSHEQDHPACHRIASLAEFALSIREVAHESNTNIFFSPVSIATAFAMLS 84

QY 66 LGTKADTHDEILGLNLFNLQIPEAQIHGFOELLRLTLNQPSQQLQTLTGNGLFLSQGLK 125
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 85 LGAKGDTHITQVLEGLKFNLTETAEQIHGDFRLLHTVNRPDSELQALAAAGNALVVHENLK 144

QY 126 LVDKFLFEDVKVLHSEATVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDVTVALV 185
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 145 LQHKFLEDAKNLQSEAFLVDFRDPQAKTKINSHVEKGTGRGKIVDLVQELDARTLLAV 204

QY 186 NYLFEKQWERPEVKDTEEDFHVDQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYL 245
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 205 NYVFFKQKWEKPEPENTKEEDFHVDATTVRVPMMSRLGMVNFHCSTLAVTLRNDYK 264

QY 246 GNATAIFFLPDEGKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTVDKLSVLGQ 305
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 265 GNATALFLLPDEGKLOHLEDTLTETELIAKFLAKLSRSVTVRFPKLSISGTYNLKVLSP 324

QY 306 LGTKVFSNGADLSGVTEAPLKSVAHVKAULTIDEKTEAAGAMFLERIPRSIPPEVK 365
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 325 LGITQVFSNNADLSGITEQBPQKLVSOALHKAVLTIDERGTEAAGAFVELIPESVPDSIT 384

QY 366 FNKPFVFLMIEQNTKSPFLFMGVNPT 392
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 385 LDRPFLFVIYSHEIKSPFLFVGKVNPT 411
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RESULT 9

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I49470
alpha-1 proteinase inhibitor 1 - mouse
N:Alternate names: alpha-1-antitrypsin
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R:Accession: I49470; A25495
R:Porriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A:Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary diver
A:Reference number: I49470; MUID:92052104; PMID:1946354
A:Accession: I49470
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-413 <RES>
A:Cross-references: UNIPROT:P07758; GB:M75721; NID:g191841; PIDN:AAC28869.1; PID:g191842
DNA 5, 29-36, 1986
R:Krauter, K.S.; Citron, B.A.; Hsu, M.T.; Powell, D.; Darnell Jr., J.E.
A:Title: Isolation and characterization of the alpha-1-antitrypsin gene of mice.
A:Reference number: A25495; MUID:86163765; PMID:3007061
A:Accession: A25495
A:Molecule type: mRNA
A:Residues: 211-245, 'D', 247-322, 'L', 324-403, 'V', 405-413 <KRA>
A:Cross-references: GB:M12586; NID:g192092; PIDN:AAA51624.1; PID:g192094
C:Genetics:
C:Gene: alpha-1 PI-1
C:Superfamily: Serpin

Query Match 65.3%; Score 1327; DB 2; Length 413;
Best Local Similarity 64.1%; Pred. No. 1.9e-84;
Matches 248; Conservative 70; Mismatches 67; Indels 2; Gaps 2;

QY 9 OKTDTSHDDHPTFNKIPNLAEPAFSLYROLAHOQSNSTNIFFSPVSIATAFAMLSLGT 68
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 28 QETDTSQKQDS-PASHEIATNLGDFALSYRELVSQSNSTNIFFSPVSIATAFAMLSLGS 86

QY 69 KADTHDEILGLNLFNLQIPEAQIHGFOELLRLTLNQPSQQLQTLTGNGLFLSQGLKLV 128
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 87 KGDTHITQVLEGLQFNLTQTSSEADIHKSFOHLLQTLNRPDSELQSLSTGNGLFVNNDLKLVE 146

QY 129 KFLQDVVKLYHSEATVNFQDTEQAKQINDYVEKGTQGIKIVDLVKELDRDVTVALVNYI 188
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 147 KFLSEAKNHYQAEVFSVNPFAESEAKKVINDFVEKGTQGIKIAEAVKCLQDQTVFALANYI 206

QY 189 FFKGKWERPEVKDTEEDFHVDQVTVKVPMMKRLGMFNIQHCCKLSSWVLLMKYLGNA 248
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 207 LFKGKWKPEPDENTEEAEFHVDESTTVKVPMMTISGMLHVHHCSTLSSWVLLMDYAGNA 266

QY 249 TAIFFLPDQKLOHLENLTHDIIITKFLNEDRRSASLHLPKLSITGTVDKLSVLGQLGI 308
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 267 TAVFLPDDQKQOHLQETLSKELSKFLNRRRLAQIHFPRLSISGEYNLKTMSPLGI 326

QY 309 TKVFSNGADLSGVTEER-APLKLKSAHVKAULTIDEKTEAAGAMFLERIPRSIPPEVKFN 367
|||:|||||:|:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
Db 327 TRIFNNGADLSGITEENAPLKLQSAHVKAULTIDETGTETAAAATVLMQVPMSPMLTRFD 386

QY 368 KPVFLMIEQNTKSPFLFMGVNPTGK 394
|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db 387 HPFLFIIEHTQSPFLFVGKVDPTHK 413

RESULT 10
JX0154
alpha-1-antiprotease F - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
R:Accession: JX0154
R:Saito, A.; Sinohara, H.
J. Biochem. 109, 158-162, 1991
A:Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiprotease F: amin
A:Reference number: JX0154; MUID:91201273; PMID:2016265
A:Accession: JX0154
A>Status: preliminary
```

A:Molecule type: mRNA
A:Residues: 1-413 <SAI>
A:Cross-references: UNIPROT:P23035; GB:X57710; NID:g1455; PIDN:CAA0881.1; PID:g1456
C:Superfamily: Serpin

Query Match 65.1%; Score 1322; DB 2; Length 413;
Best Local Similarity 64.3%; Pred. No. 4.2e-84;
Matches 249; Conservative 63; Mismatches 75; Indels 0; Gaps 0;

Qy 6 DAAQTDTSHHQDHPFNKITNLAEFAFSLYRQLAQHSNSTNIFFSPVSIATAFAMLS 65
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 25 DEAQETAVSHEQDHPACHRIAPSLAEFALSLEYVAHESNTNIFFSPVSIATAFAMLS 84
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 66 LGTKADTHDEILLEGINFLNLTQIPRAQHGFQEELLRTLNQPSQLQTTGNGLPLSQGLK 125
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 85 LGAKGDTHTQVLEGLKENLTETAERAIHQDFGRHLLHTVNRPDSELQAARNALVWHENLK 144
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 126 LVQKFLEDVKKLHYHSEAFPTNFGTEOAKQINDYVEKGTCQGKIVDLAVKELDRDTPVALY 195
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 145 LQHKFLSDAKNLYOSEAPLVDFRPEQAKTKINSHVBKGTGRGKIVDLVQELDARTLLAY 204
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 186 NYIFFKGKWRPFVKDTEBEDFHVDQVTTVKVPMKRGLGMFNIOHQCKLSWVLLMKYL 245
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 205 NYVFFKGKWEKPPENTKEEDFHNATTTVRVPMKSELGRYDLFHCSTIASVLRLMDYK 264
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 246 GNATAIFFLPDEGKLOHLENELTHDIITKPLENEDRRSASLIHLPKLSITCTYDLKSVLGQ 305
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 265 GNATALPLLDEGKLOHLEDTLTTELITKFLAKSSLRSVTVHPFKLSISGYDYDLKPLLKG 324
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 306 LGITKVPNSGADLSGVTEEARPLKSKAVHKAVLTIDEGCTEAGAMEFLERIPIRSIPPEVK 365
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 325 LGITQVFSDNADLSGITGEQBPLKASQALRKAVLTIDERGTEAAGATYMEIIPMSLPDSIT 384
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 366 FNKPFEVFLMTIEQNTKSLFMGKVVNP 392
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 385 LDRPFLVIYSHEIKSPLFVGKVVDP 411
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 11
I49471
alpha-1 proteinase inhibitor 2 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I49471
R:Borriello, F.; Krauter, K.S.
A>Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary divergence
A:Reference number: I49470; MUID:92052104; PMID:I4946354
A:Accession: I49471
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: mRNA
A:Residues: 1-402 <RES>
A:Cross-references: UNIPROT:P22599; GB:M75716; NID:g191843; PIDN:AAC28865.1; PID:g191844
C:Genetics:
A:Gene: alpha-1 PI-2
C:Superfamily: Serpin

Query Match 65.0%; Score 1321; DB 2; Length 402;
Best Local Similarity 64.1%; Pred. No. 4.7e-84;
Matches 248; Conservative 69; Mismatches 68; Indels 2; Gaps 2;

Qy 9 QKTDTSHHDQDHPFNKITNLAEFAFSLYRQLAQHSNSTNIFFSPVSIATAFAMLSIGT 68
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 17 QETDTSQKDQS-PASHKIATNLGDAFSLRYELVHQSNSTNIFFSPVSIATAFAMLSLGS 75
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 69 KADTHDEILLEGINFLNLTQIPRAQHGFQEELLRTLNQPSQLQTTGNGLPLSQGLKLV 128
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 76 KGDTHTQILEGLQPNLTQTSADIIHKSFOHLLQTLNRPDSELQLSTGNGLFVNNDKLIVE 135
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 129 KFLEDVKKLHYHSEAFPTNFGTEOAKQINDYVEKGTCQGKIVDLVYKELDRDTPVALNYI 188
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 136 KFLFEAKNHQAEVFSYNFAESEAKVINDFVEKGTQGIKVEAVKELDDQTVFALANYI 195
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Db 327 TRIFNCGADLSGITEENAPLKLKAVHKAVLTIDETCTEAAAATVLQVATYSMPPIVRED 386

Qy 368 KPFVFLMIEONTKSPLFMGKRVNPTGK 394

Db ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||||
387 HPFLFIIFEHTQSPIFVGVKVDPTHK 413

Search completed: June 20, 2005, 19:46:41
Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:34:59 ; Search time 172 Seconds
(without alignments)
1173.019 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPQDAQKTSTSHDQD.....IEQNTKSPFMGKVNPTCK 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2003	98.6	418	1	ALAT HUMAN
2	1883	92.7	396	2	O00394
3	1870	92.0	409	1	ALAT PAPAN
4	1701	83.7	370	2	O86U18
5	1472.5	72.5	412	1	ALAT CALCN
6	1462	71.9	309	2	O86U19
7	1459.5	71.8	421	1	ALAT PIG
8	1458	71.8	413	2	O54761
9	1443.5	71.0	411	1	ALAT RAT
10	1443.5	71.0	411	2	O6AYZ5
11	1440.5	70.9	421	2	O46519
12	1431.5	70.4	413	2	P97277
13	1430	70.4	416	1	ALAT SHEEP
14	1427	70.2	413	1	ALMT_TAMSI
15	1414	69.6	413	2	O76HPO
16	1409	69.3	416	1	ALAT BOVIN
17	1383	68.1	413	1	ALST_TAMSI
18	1379	67.9	413	1	ALST_TAMSI
19	1372	67.5	413	2	O76HN9
20	1362	67.0	413	1	ALMS_TAMSI
21	1352	66.5	406	2	O64118
22	1335	65.7	413	2	O28665
23	1327	65.3	413	1	ALTI_MOUSE
24	1327	65.3	413	2	O8VC20
25	1327	65.3	413	2	O76HP1
26	1326	65.3	410	2	O91WH5
27	1326	65.3	413	2	O91V74
28	1326	65.3	413	2	O91XB8
29	1326	65.3	422	2	O80YB8
30	1322	65.1	413	1	ALAP_RABIT
31	1322	65.1	425	2	O91XCI

32	1321	65.0	413	1	ALT3_MOUSE
33	1320	65.0	413	1	ALT2_MOUSE
34	1316	64.8	413	2	O8VC41
35	1315	64.7	413	2	O07298
36	1314	64.7	456	2	O62663
37	1310	64.5	413	1	ALT4_MOUSE
38	1301	64.0	413	1	HP55_TAMSI
39	1298	63.9	413	2	Q28666
40	1296	63.8	413	2	O63969
41	1294	63.7	413	1	ALT5_MOUSE
42	1281.5	63.1	412	1	ALAT_MUSCR
43	1280	63.0	405	1	ALAS_CAVPO
44	1280	63.0	413	2	O54762
45	1260	62.0	403	1	ALAP_CAVPO
46	1235	60.8	410	1	COTR_CAVPO
47	1168	57.5	413	2	O91X22
48	1153.5	56.8	410	1	ALAT DIDMA
49	1125	55.4	420	1	ALAU_HUMAN
50	1012	49.8	433	2	O9Y1B8
51	1007.5	49.6	432	2	O7SYX0
52	1004	49.4	197	2	Q13747
53	1001	49.3	431	2	O66KX6
54	946	46.6	426	2	O8JIA6
55	839.5	41.3	420	2	O60552
56	834	41.0	410	2	O90323
57	833	41.0	407	2	O9UNU9
58	833	41.0	423	1	AACT_HUMAN
59	829	40.8	406	1	IPSP_HUMAN
60	828	40.7	411	2	O9TTE1
61	824	40.6	418	1	COTR_MOUSE
62	824	40.6	418	2	O91X80
63	823	40.5	418	2	O8VCH3
64	822	40.5	418	2	O03734
65	821.5	40.4	415	2	O9GMA6
66	820	40.4	418	2	O91W80
67	819	40.3	427	1	KAIN_HUMAN
68	819	40.3	445	2	O86TR9
69	813.5	40.0	416	2	O6P6G8
70	813.5	40.0	426	2	O722W1
71	813	40.0	435	1	CBG_HUMAN
72	811.5	39.9	405	1	CBG_HUMAN
73	810.5	39.9	405	2	O722Q9
74	807	39.7	418	2	O62257
75	806	39.7	406	1	CBG_SALSC
76	804.5	39.6	416	1	CP11_RAT
77	804.5	39.6	418	2	O91WP6
78	804	39.6	383	1	CBG_RABIT
79	804	39.6	440	2	O86U17
80	803.5	39.5	418	2	O62258
81	803	39.5	418	1	CP16_RAT
82	802	39.5	413	1	CP13_RAT
83	797	39.2	430	1	CBG_SHEEP
84	796.5	39.2	412	1	THBG_PIG
85	795	39.1	404	2	O9N2I2
86	793	39.0	417	1	KBP_MOUSE
87	791	39.0	414	2	O8IW75
88	788.5	38.7	418	1	THBG_MOUSE
89	786.5	38.7	412	1	THBG_SHEEP
90	783	38.5	471	2	O80X76
91	782.5	38.5	411	1	THBG_BOVIN
92	781.5	38.5	415	1	THBG_HUMAN
93	780.5	38.4	405	1	IPSP_MOUSE
94	776.5	38.2	415	1	THBG_PANTR
95	775.5	38.2	406	2	O88292
96	772.5	38.0	406	2	O66HL5
97	771.5	38.0	418	1	SI24_APOSY
98	771.5	38.0	418	1	THBG_RAT
99	767.5	37.8	405	2	O8BU50
100	765.5	37.7	424	2	O8CIE0

ALIGNMENTS


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QY 181 VFALVNYIFFKQKWERPFVEKDTBEDHFVDQVTVTKVPMKRLGMFNIQHCKKLSWYL 240
Db 183 VFALVNYIFFKQKWERPFVEATKEBDFHVDQATTVTKVPMRRLGMFNIYHCKKLSWYL 242
QY 241 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENEDRRSASLHLPKLSITGTGYDLK 300
Db 243 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENENRRSANLHLPKLSITGTGYDLK 302
QY 301 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVALTIDEGTEAAGAMFLERIPRSI 360
Db 303 TVLGHGKITKVFSGNADLSGVTEADAPLKLKSKAVHKAVALTIDEGTEAAGAMFLERIPRSI 362
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 363 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 396

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RESULT 3

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ALAT_PAPAN STANDARD; PRT; 409 AA.
ID ALAT_PAPAN PRELIMINARY; PRT; 370 AA.
AC P01010;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease) (AAT) (Fragment).
GN Name=SERPIN1; Synonyms=PI;
OS Papio anubis (olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82082539; PubMed=7031661;
RA Kurchi K., Chandra T., Friezen Degen S.J., White T.T.,
RA Marchioro T.L., Woo S.L.C., Davie E.W.;
RT "Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).
CC -!- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC elastase, but it also has a moderate affinity for plasmin and
CC thrombin.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; J00321; AAA35377.1; -.
CC DR HSSP; P01009; 1EZX.
CC DR InterPro; IPR000215; Prot_inh_serpin.
CC DR Pfam; PF00079; Serpin; 1.
CC DR SMART; SM00093; SERPIN; 1.
CC DR PROSITE; PS00284; SERPIN; 1.
CC KW Acute phase; Glycoprotein; Plasma; Serine protease inhibitor; Serpin;
CC Signal.
CC FT NON_TER 1 1
CC FT SIGNAL <1 15
CC FT CHAIN 16 409 Alpha-1-antitrypsin.
CC FT SITE 373 374 Reactive bond.
CC FT CARBOHYD 61 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 262 262 N-linked (GlcNAc...) (Potential).
CC SEQUENCE 409 AA; 45694 MW; E1980B7450FDBA9B CRC64;

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Query Match 92.0%; Score 1870; DB 1; Length 409;

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Best Local Similarity 91.1%; Pred. No. 2.5e-116;
Matches 359; Conservative 21; Mismatches 14; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYROLAHQSNSTNIFSPVSIATA 60
Db 16 EDPOGDAQAQKTDTPPHDQNHPTLNKITPSLAFAFSLYROLAHQSNSTNIFSPVSIATA 75
QY 61 FAMLISGTKADTHDEILEGINFNLTQIPRAQIHEGFQELLRLTNOPDSQLQTTGNGLFL 120
Db 76 FAMLISGTKADTHSELGLNFNLTEIPRAQVHEGFQELLRLTNKPEDSQLQTTGNGLFL 135
QY 121 SQGLKLVDPKFLVDVKKLYHSEAFNFTNGTEQAQKQINDYVEKGTQGKIVDLVKELDRDT 180
Db 136 NKSLKLVDPKFLVDVKKLYHSEAFNFTNGTEQAQKQINDYVEKGTQGKIVDLVKELDRDT 195
QY 181 VFALVNYIFFKQKWERPFVEKDTBEDHFVDQVTVTKVPMKRLGMFNIQHCKKLSWYL 240
Db 196 VFALVNYIFFKQKWERPFVEATEBEDHFVDQATTVKVPMMRRLGMFNIYHCKKLSWYL 255
QY 241 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENEDRRSASLHLPKLSITGTGYDLK 300
Db 256 LMKYLGNAITAFPLPDEGKQHLLENELTHDITTKFLENENRRSANLHLPKLSITGTGYDLK 315
QY 301 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVALTIDEGTEAAGAMFLERIPRSI 360
Db 316 TVLGHGKITKVFSGNADLSGVTEADAPLKLKSKAVHKAVALTIDEGTEAAGAMFLERIPRSI 375
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 376 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 409
RESULT 4
Q85U18 PRELIMINARY; PRT; 370 AA.
ID Q86U18;
AC Q86U18;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DM003YH14 of Fetal liver of Homo sapiens
DE (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; BX248257; CAD62585.1; -.
DR HSSP; P01009; 8API.
DR GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
FT NON_TER 1 1
SQ SEQUENCE 370 AA; 41448 MW; 024F8B34B600E204 CRC64;
Query Match 83.7%; Score 1701; DB 2; Length 370;
Best Local Similarity 99.1%; Pred. No. 3.8e-105;
Matches 328; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYROLAHQSNSTNIFSPVSIATA 60
Db 36 EDPOGDAQAQKTDTHSHDQDHPFNKITPNLAFAFSLYROLAHQSNSTNIFSPVSIATA 95

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QY 61 FAMSLSGTADTHDEILLEGLENFNLTQIPPAQIHGFGFOLLRTLNQPPSQQLQTLTGNGLFL 120
Db 96 FAMSLSGTADTHDEILLEGLENFNLTQIPPAQIHGFGFOLLRTLNQPPSQQLQTLTGNGLFL 155
QY 121 SOGLKLVDFKLEVDKLYHSEAFVNFPGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 156 SEGKLVDFKLEVDKLYHSEAFVNFPGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDT 215
QY 181 VFALVNYIPFKGKWERPFVEKDTSEEDFHVDTQVTVTKVPMKRLGMFNIQHCCKLSSWVL 240
Db 216 VFALVNYIPFKGKWERPFVEKDTSEEDFHVDTQVTVTKVPMKRLGMFNIQHCCKLSSWVL 275
QY 241 LMKYLGNATAIFLDPBCKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLK 300
Db 276 LMKYLGNATAIFLDPBCKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLK 335
QY 301 SVLGQGITKVFSGNADLSGVTEAPLKLK 331
Db 336 SVLGQGITKVFSGNADLSGVTEAPLKLK 366

RESULT 5
ALAT_CALCIN STANDARD; PRT; 412 AA.
AC Q54783;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-1-antiprotease precursor (Alpha-1-antitrypsin) (Alpha-1-
proteinase inhibitor).
OS Callosciurus caniceps (Gray-bellied squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriidae; Scurinae;
OC Callosciurus.
OX NCBI_TaxID=64664;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9431474; DOI=10.1016/S0378-1119(97)00532-5;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Teutou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alpha1-antitrypsin-like genes in hibernating
RT species of the squirrel family."
RL Gene 204:127-132(1997).
CC -!- FUNCTION: Inhibitor of serine proteases (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB000552; BAA24422.1; -.
DR HSSP; P01009; IQMB.
DR InterPro; IPR000215; Prot_inh_serpin.
DR PFAM; PF000079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Acute phase; Glycoprotein; Plasma; Serine protease inhibitor; Serpin;
KW Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 412 Alpha-1-antiprotease.
FT SITE 377 378 Reactive bond (By similarity).
FT CARBOHYD 65 65 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
```

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SQ SEQUENCE 412 AA; 45729 MW; 7235668E9EB8FCC6 CRC64;
Query Match 72.5%; Score 1472.5; DB 1; Length 412;
Best Local Similarity 72.7%; Pred. No. 7.2e-90;
Matches 282; Conservative 46; Mismatches 59; Indels 1; Gaps 1;
QY 5 GDAQAQTDTHSHDQDPTFNKIPNLAEPAFSLYROLAHSNSTNIFFSVSTATAFAML 64
Db 25 GD-AQETDASAKDDEHPACHKAPNLAEPAFSLYRLARQSNNTNIFFSVSTATAFAML 83
QY 65 SLGTADTHDEILLEGLENFNLTQIPPAQIHGFGFOLLRTLNQPPSQQLQTLTGNGLFLSOGL 124
Db 84 SLGTADTHDEILLEGLENFNLTQIPPAQIHGFGFOLLRTLNQPPSQQLQTLTGNGLFLSOGL 143
QY 125 KLVDKLEVDKLYHSEAFVNFPGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDTVPAL 184
Db 144 KLADKLEVDKLYHSEAFVNFPGDTEQAKQINDYVEKGTQGIKIVDLVKELDRDTVPAL 203
QY 185 VNYIPFKGKWERPFVEKDTSEEDFHVDTQVTVTKVPMKRLGMFNIQHCCKLSSWVLKMY 244
Db 204 VNYIPFKGKWERPFVEKDTSEEDFHVDTQVTVTKVPMKRLGMFNIQHCCKLSSWVLKMY 263
QY 245 LGNATAIFLDPBCKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLKSVLG 304
Db 264 LGNATAIFLDPBCKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYVDLKSVLG 323
QY 305 QLGITKVFSGNADLSGVTEAPLKLKSKAVHKAIVLITDERGTEAAGAMFLERIPRSIPPEV 364
Db 324 TLGITKVFSGNADLSGVTEAPLKLKSKAVHKAIVLITDERGTEAAGAMFLERIPRSIPPEV 383
QY 365 KFNKPFVFLMIRQNTKSPFMKGVNPT 392
Db 384 RFDRLPLIIHYHYTKSPFLFVGKVNPT 411

RESULT 6
Q86U19 PRELIMINARY; PRT; 309 AA.
AC Q86U19;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Full-length cDNA clone CS0DM003YH10 of Fetal liver of Homo sapiens
DE (human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal liver;
RA Genoscope;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the serpin family.
DR EMBL; BX248002; CAD62334.1; -.
DR HSSP; P01009; BAPI.
DR GO; GO:004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR PFAM; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
KW NON_TER 1
FT SEQUENCE 309 AA; 35116 MW; 5AF00026C06FBE9E CRC64;
Query Match 71.9%; Score 1462; DB 2; Length 309;
Best Local Similarity 98.9%; Pred. No. 2.5e-89;
Matches 279; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 EDPOGDAQAQKTDTSRHDQDHPFNKITTPLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA 60
Db 28 EDPOGDAQAQKTDTSRHDQDHPFNKITTPLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA 87
QY 61 FAMLISGTTKADTHDEILEGNFNLTOIPRAQIHEGFQELLRLTNQDPSQLQTLTNGLFL 120
Db 88 FAMLISGTTKADTHDEILEGNFNLTOIPRAQIHEGFQELLRLTNQDPSQLQTLTNGLFL 147
QY 121 SOGLKLVDFLEDDVKLYHSEAFVNFNGTEQAOKQINDYVEKGTGQKIVDLVKELDRDT 180
Db 148 SEGKLVDFLEDDVKLYHSEAFVNFNGTEQAOKQINDYVEKGTGQKIVDLVKELDRDT 207
QY 181 VFALVNYIIFFGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWYL 240
Db 208 VFALVNYIIFFGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWYL 267
QY 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIIITKFLFLENEDRR 282
Db 268 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIIITKFLFLENEDRR 309

RESULT 7
ALAT_PIG STANDARD; PRT; 421 AA.
ID ALAT_PIG AC P50447;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
DE antiprotease).
GN Name=SERPINAl; Synonyms=PI;
OS Sus scrofa (Pig).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97009792; PubMed=8856896;
RA Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
RA Gellin J.;
RT "Porcine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and
RT assignment to chromosome 7q2.4-q2.6.";
RL Anim. Genet. 27:85-89(1996).
CC -I- FUNCTION: Inhibitor of serine proteases. Its primary target is
CC elastase, but it also has a moderate affinity for plasmin and
CC thrombin (by similarity).
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- SIMILARITY: Belongs to the serpin family.
CC -----
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CC -----
DR EMBL; X88780; CAA61259.1; -.
DR HSSP; P01009; 1QMB.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Glycoprotein; Plasma; Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 24 Potential.
FT CHAIN 25 421 Alpha-1-antitrypsin.
FT SITE 385 386 Reactive bond.
FT CARBOHYD 73 73 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 421 AA; 47194 MW; 08A4AB2A9E600890 CRC64;

Query Match 71.8%; Score 1459.5; DB 1; Length 421;
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Best Local Similarity 72.0%; Pred. No. 5.4e-89;
Matches 286; Conservative 40; Mismatches 68; Indels 3; Gaps 1;

QY 1 EDPOGDAQAQKTDTSRHDQD---HPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSI 57
Db 25 EGLQGHAVQETDPRPHDHEHQHQAACHRIAPNLADFASLYRQVARQSNSTNIFLSPVTI 84
QY 58 ATAFAMLSIGTTKADTHDEILEGNFNLTOIPRAQIHEGFQELLRLTNQDPSQLQTLTNG 117
Db 85 ARAFAMLSIGTTKAGATHAEILEGLQNLTEKAEAEIHEGFQHLHLTLNQPDNLQTLTNG 144
QY 118 LFLSGLKLVDFLEDDVKLYHSEAFVNFNGTEQAOKQINDYVEKGTGQKIVDLVKELD 177
Db 145 LPIDEKAKLVPRFLEDDVKNLHYSEAFSNFRDTEEAKKINDYVEKSGQKIVDLVDLD 204
QY 178 RDTVFALVNYIIFFGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLS 237
Db 205 KDTVFALVNYIIFFGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLS 264
QY 238 WYLLMKYLGNAATAIFFLPDEGKLOHLENELTHDIIITKFLFLENEDRRSASLHLPKLSITGY 297
Db 265 WYLLMDYVATATAFFILPDQGKLHQLDMLTKAIRAKPLEKRYPPSSANLHLPKLSITGY 324
QY 298 DLKSVLGQIGITKVPFSGADLSGVTEAPLKLKSKAVHKAVALIIDKGTGAAGAMFLERIP 357
Db 325 DLKSLGLNGLITKVPFSDADLSGVTEEQPLKLSKALHRAVLTIDEKGTGATATILEAIP 384
QY 358 RSIPPEVFNKPFVFLMTEQNTKSPLEMGKVVNPTGK 394
Db 385 MSIPPNVFNKPFVFLIYDTKTKAFLFMGKVMNPQK 421

RESULT 8
OS4761 PRELIMINARY; PRT; 413 AA.
ID OS4761;
AC OS4761;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Alpha, antitrypsin-like protein.
OS Sperophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Sperophilus.
OX NCBI_TaxID=43179;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98094263; PubMed=9434174; DOI=10.1016/S0378-1119(97)00532-5;
RA Takamatsu N., Kojima M., Taniyama M., Ohba K., Uematsu T., Segawa C.,
RA Tautou S., Watanabe M., Kondo J., Kondo N., Shiba T.;
RT "Expression of multiple alaphal-antitrypsin-like genes in hibernating
RT species of the squirrel family.";
RL Gene 204:127-132(1997).
CC -I- SIMILARITY: Belongs to the serpin family.
DR EMBL; AB000550; BAA24420.1; -.
DR HSSP; P01009; 1QMB.
DR GO; GO:0004867; F_serine-type endopeptidase inhibitor activity; IEA.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Protease inhibitor; Serine protease inhibitor; Serpin.
SQ SEQUENCE 413 AA; 45953 MW; B08D2544695EE0F4 CRC64;

Query Match 71.8%; Score 1458; DB 2; Length 413;
Best Local Similarity 71.2%; Pred. No. 6.6e-89;
Matches 274; Conservative 56; Mismatches 55; Indels 0; Gaps 0;

QY 8 AOKTDTSHDQDHPFNKITTPLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSIG 67
Db 27 AOKTGSKHDQEHPSHRIAPNLAEFALSLYRVLAEHSNTNIFLSPVSIAMALASLIG 86
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QY 68 TKADTHDEILGCLNFTNLTQIPRAQIHGFGQELLTLNQPDSQLOLTTGNGLFLSQGLKLV 127
Db 87 TKADTHTHQIMIEGGLNLTAEASIHQGFQELLQTLNKNPSQLOLTTGNGLFLDHNKLL 146
QY 128 DKFLEDVKLYHSAFTVNFQDTEOAKQINDVVEKGTQCKIVDLVKELDRDTVFALVNY 187
Db 147 DKFLODVKNLYHSAFTDNTNTEAKQINTVVEKGTQCKIVDLVKELDRDVSVALVNY 206
QY 188 IFPKGKWERPFVKOTBEEDFHVDQVTVTKVPMKRLGMFNIQHCCKLSSWVLLMKYLG 247
Db 207 IFPKGKWKPEFVDHTKEEDFHVDQVTVTVPMNRMGMPEVHYCSTLASWVLQMDYLG 266
QY 248 ATAIFPLPDGKLOHLENELTHDIITKFLNEEDRSASLHLPKLSITGTVDLKSVLGQIG 307
Db 267 ATAIFLLPDGKLOHLEDDITKILAKFLKNRSSVNLHFPKLNISGTVMDLKPVLTRLG 326
QY 308 ITKVFNSGADLSGVTEAPKLSKAVHKAVLTIDKGTGAAGAMFLERIPRSIPPEVKFN 367
Db 327 ITNVFSYKADLSGITEDDPLRVQALHKAVALTIDERGTEAAGATFLEMMPMSIPPEVKFD 386
QY 368 KPFVFLMIEQNTKSPPLFMGKVNPVT 392
Db 387 KPFLVWIIHSTKSPFLFVGKVNPVT 411

RESULT 9
ALAT_RAT STANDARD; PRT; 411 AA.
AC P17475;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-1-antitrypsin precursor (Alpha-1-antitrypsin) (Alpha-1-
DE proteinase inhibitor).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE OF 4-411 FROM N.A., AND SEQUENCE OF 25-57.
RC TISSUE=Liver;
RX MEDLINE=90148955; PubMed=2302382;
RA Chao S., Chai K.X., Chao L., Chao J.;
RT "Molecular cloning and primary structure of rat alpha 1-antitrypsin.";
RL Biochemistry 29:323-329(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=91035351; PubMed=2229024;
RA Misumi Y., Sohda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
RT "Molecular cloning and sequencing of the cDNA of rat alpha 1-protease
RT inhibitor and its expression in COS-1 cells.";
RL J. Biochem. 108:230-234(1990).
RN [3]
RP SEQUENCE OF 188-389 FROM N.A.
RC TISSUE=Liver;
RA Flink I.L., Bailey T., Morkin E.;
RL Submitted (AUG-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Inhibitor of serine proteases. The primary target is
CC elastase, but also has a moderate affinity for plasmin and
CC thrombin.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the serpin family.
CC
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DR EMBL; M32247; AAA40788.1; --
DR EMBL; D00675; BAA00579.1; --
DR EMBL; X16273; CAA34349.1; --
DR PIR; A33892; ITRT.
DR HSP; P01009; IOMB.
DR InterPro; IPR000215; Prot_inh_serpin.
DR Pfam; PF00079; Serpin; 1.
DR SMART; SM00093; SERPIN; 1.
DR PROSITE; PS00284; SERPIN; 1.
KW Direct protein sequencing; Glycoprotein; Plasma;
KW Serine protease inhibitor; Serpin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 411 Alpha-1-antitrypsinase.
FT SITE 376 377 Reactive bond.
FT CARBOHYD 64 64 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 101 101 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 265 265 N-linked (GlcNAc...) (Potential).
FT CONFLICT 14 14 A -> G (in Ref. 2).
FT CONFLICT 84 84 L -> V (in Ref. 2).
FT CONFLICT 247 247 M -> I (in Ref. 3).
FT CONFLICT 248 248 H -> Y (in Ref. 2).
FT CONFLICT 318 318 K -> N (in Ref. 2).
FT CONFLICT 322 322 S -> D (in Ref. 3).
SQ SEQUENCE 411 AA; 46135 MW; B4245CFE21C5C761 CRC64;

Query Match 71.0%; Score 1443.5; DB 1; Length 411;
Best Local Similarity 69.9%; Pred. No. 6.1e-88;
Matches 269; Conservative 62; Mismatches 53; Indels 1; Gaps 1;

QY 8 AQKTDTHSHDQDHPNTFNKLTNLAFAFSLYROLAHQSNTNFFSPVSTATAFAMLSLG 67
Db 27 AQETDTSQDQS--PTYRKISSNLADFAFSLYRELHVQSNTNFFSPMSITTAFAMLSLG 85
QY 68 TKADTHDEILGCLNFTNLTQIPRAQIHGFGQELLRTLNQDSQLOLTTGNGLFLSQGLKLV 127
Db 86 SKGDTKQKLEGLFELNLTQIPDAIHKAFLHLLQTLNRPDSELQMLTNGLFLVKNKLV 145
QY 128 DKFLEDVKLYHSAFTVNFQDTEOAKQINDVVEKGTQCKIVDLVKELDRDTVFALVNY 187
Db 146 EKFLERVKNYHSEAFSVNFADSEAKKINDVVEKGTQCKIVDLVKELDRDTVFALVNY 205
QY 188 IFPKGKWERPFVKOTBEEDFHVDQVTVTKVPMKRLGMFNIQHCCKLSSWVLLMKYLG 247
Db 206 IFPKGKWKPEFVDHTKEEDFHVDKSTTVKVPMMNRLGMFDMHYCSTLSSWVLLMDYLG 265
QY 248 ATAIFPLPDGKLOHLENELTHDIITKFLNEEDRSASLHLPKLSITGTVDLKSVLGQIG 307
Db 266 ATAIFLLPDGKMOHLEQLTKDLISRFNLNRTSRALIFPKLSISGTYNLKLTLSLG 325
QY 308 ITKVFNSGADLSGVTEAPKLSKAVHKAVLTIDKGTGAAGAMFLERIPRSIPPEVKFN 367
Db 326 ITRVFNNDADLSGITEDAPKLSQAVHKAVLTIDERGTEAAGATVVEAVPMSPVPPVKFD 385
QY 368 KPFVFLMIEQNTKSPPLFMGKVNPVT 392
Db 386 HPFIFMIVESETQSPFLFVGKVDPVT 410

RESULT 10
Q6AYZ5 PRELIMINARY; PRT; 411 AA.
AC Q6AYZ5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Serine protease inhibitor alpha 1.
GN Name=Serpinal;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.

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RN  SEQUENCE FROM N.A.
RP  TISSUE=Liver;
RC  MEDLINE=96004896; PubMed=7548212; DOI=10.1016/0167-4781(95)00140-C;
RA  Nakatani T., Suzuki Y., Yoshida K., Sinohara H.;
RX  "Molecular cloning and sequence analysis of cDNA encoding plasma
RT  alpha-1-antitrypsinase from Syrian hamster: implications for the
RT  evolution of Rodentia.";
RL  Biochem. Biophys. Acta 1263:245-248 (1995).
CC  -1- SIMILARITY: Belongs to the serpin family.
DR  ENBL; D49709; BAA08557.1; -.
DR  PIR; S60036; S60036.
DR  HSSP; P01009; IQMB.
DR  GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
DR  InterPro; IPR000215; Prot_inh_serpin.
DR  Pfam; PF00079; Serpin; 1.
DR  SMART; SM00093; SERPIN; 1.
KW  Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
FT  SIGNAL 1 24 Potential.
FT  CHAIN 25 413 alpha-1-antitrypsinase.
SQ  SEQUENCE 413 AA; 45819 MW; 71D192E106A1EB36 CRC64;

Query Match 70.4%; Score 1431.5; DB 2; Length 413;
Best Local Similarity 70.2%; Pred. No. 3.9e-87;
Matches 271; Conservative 55; Mismatches 59; Indels 1; Gaps 1;

QY 8 AQKTDTHSHDQDHPFTFNKITPNLAEPFSLYRQLAQHSNSTIFFSPVSIATAFAMLSLG 67
DB 27 AQETDASKQDQEQHQAQCKKIAPNLADSFNLYRELHQSNSTIFFSPVSIATAFAMLSLG 86
QY 68 TKADTHDEILGLGNFNLTPQIAQIHGEGQELLRTLNQDPSQLQTTGNGFLSQGLKLV 127
DB 87 TKGVTHTQLEGLGFLNLTAEAEVHKGFNLQTFNRPNEQLQTTGNGFLTHNNKLV 146
QY 128 DKFLEDVKKLYHSEAFVFNPGDTEQAQKQINDVVEKGTQKIVDLVKELDRDTPFALVNY 187
DB 147 DKFLEEVKNDYHSEAFVFNPGDTEQAQKQINDVVEKGTQKIVDLVKELDRDTPFALVNY 206
QY 188 IFFPKGWRPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIQHKCKLSWLLMKYLG 247
DB 207 IFFPKGWRPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIQHKCKLSWLLMKYLG 266
QY 248 ATAIFLPEDEKQHLNETHDIITKPLENEDRSASLHLPKLSITGYDLSVQLG 307
DB 267 ATAIFLPEDEKQHLNETHDIITKPLENEDRSASLHLPKLSITGYDLSVQLG 326
QY 308 ITKVFNSGADLSGVTEEPKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSIPPE 367
DB 327 ITKVFNSGADLSGVTEEPKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSIPPE 386
QY 368 KPFVFLMIEQNT-KSLPFGKVVNPT 392
DB 387 SPIAIYDRQTAQKSPFLVGVKVDPT 412

RESULT 13
ALAT SHEEP
ID ALAT SHEEP STANDARD; PRT; 416 AA.
AC P12725;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Alpha-1-antitrypsinase precursor (Alpha-1-antitrypsin) (Alpha-1-
OS proteinase inhibitor).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Eutelestomi;
OC Mammalia; Ruminantia; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=89366677; PubMed=2788872;

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RA Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R., Wu Y.;
RT "Nucleotide and deduced amino acid sequence of sheep alpha 1
RT antitrypsin.";
RL Nucleic Acids Res. 17:6398-6398 (1989).
RN [2]
RP SEQUENCE OF 25-55.
RC TISSUE=Plasma;
RX MEDLINE=91144555; PubMed=1899999;
RA Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.;
RT "Isolation and characterization of sheep alpha 1-proteinase
RT inhibitor.";
RL Biochem. J. 273:685-690 (1991).
CC -1- FUNCTION: Inhibits human leukocyte elastase, pig pancreatic
CC elastase and bovine trypsin on a 1:1 molar basis.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR  EMBL; X15555; CAA33561.1; -.
DR  PIR; S05312; ITSH.
DR  HSSP; P01009; IQMB.
DR  InterPro; IPR000215; Prot_inh_serpin.
DR  Pfam; PF00079; Serpin; 1.
DR  SMART; SM00093; SERPIN; 1.
DR  PROSITE; PS00284; SERPIN; 1.
KW  Direct protein sequencing; Glycoprotein; Plasma;
KW  Serine protease inhibitor; Serpin; Signal.
FT  SIGNAL 1 24
FT  CHAIN 25 416 Alpha-1-antitrypsinase.
FT  SITE 380 381 Reactive bond.
FT  CARBOHYD 68 68 N-linked (GlcNAc...) (Potential).
FT  CARBOHYD 105 105 N-linked (GlcNAc...) (Potential).
FT  CARBOHYD 143 143 N-linked (GlcNAc...) (Potential).
FT  CARBOHYD 269 269 N-linked (GlcNAc...) (Potential).
FT  CONFLICT 39 39 A -> S (in Ref. 2).
FT  CONFLICT 45 45 C -> A (in Ref. 2).
SQ  SEQUENCE 416 AA; 45984 MW; 0B4702C0527321BF CRC64;

Query Match 70.4%; Score 1430; DB 1; Length 416;
Best Local Similarity 69.2%; Pred. No. 4.9e-87;
Matches 269; Conservative 62; Mismatches 56; Indels 2; Gaps 1;

QY 4 QGDAAQKTDTHSHDQDHPFTFNKITPNLAEPFSLYRQLAQHSNSTIFFSPVSIATAFAM 63
DB 28 QGHAVQETDDTAHQE--AACHKIAPNLANFAFSIYHKLHQSNSTIFFSPVSIATAFAM 85
QY 64 LSLGKADTHDEILGLGNFNLTPQIAQIHGEGQELLRTLNQDPSQLQTTGNGFLSQGL 123
DB 86 LSLGAKGNTHTEILGLGFLNLTAEAEVHKGFNLQTFNRPNEQLQTTGNGFLPINES 145
QY 124 LKLVKFLVDKLYHSEAFVFNPGDTEQAQKQINDVVEKGTQKIVDLVKELDRDTPFA 183
DB 146 AKLVDTFLEDVKNLHSHKAFSINFRDAEBAKKINDVVEKSHGKIVDLVKELDRDTPFA 205
QY 184 LVNYIFFKGRPFVKDTEEDFHVDTQVTVKVPMMKRLGMFNIQHKCKLSWLLMK 243
DB 206 LVNYISFKGWEKPFVEHTEHDFHVNQTTVTKVPMNRLGMFNLHLYCDKLSWLLD 265
QY 244 YLGNTAIFLPEDEKQHLNETHDIITKPLENEDRSASLHLPKLSITGYDLSVQL 303
DB 266 YVGNVTACFILPDGLKQLQLEDKLNELAKFLKLYASSANLHLPKLSITGYDLSVQL 325
QY 304 GOLGITKVPNSGADLSGVTEEPKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSIPPE 363
DB 326 GELGINRVFNSGADLSGVTEEPKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSIPPE 385

```


Qy	308	ITKVFSNGADLSGVTEEA	PLKSKAVHKAVL	TIDEKGT	EAAGAMFLER	IPRSIPPEVKFN	367
Db	327	ITKVFSQADLSGVTEEA	PLTVSKGLHKA	VLDIHEKGT	DAAGATFLEM	IPMMLPSDLKFD	386
Qy	368	KPFVFLMIEONTKSP	LFMGKVNP	T			392
Db	387	RPFLVVIYEHHTKSP	LFVGVNP	T			411

Search completed: June 20, 2005, 19:45:54
Job time : 175 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:34:19 ; Search time 75 Seconds
(without alignments)
2031.781 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPOGDAQAQKDTSHDQD.....IEQNTKSLFMGKVVNPTGK 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2032	100.0	394	2	AAY44201
2	2026	99.7	394	2	AAY44205
3	2003	98.6	394	2	AAY59839
4	2003	98.6	394	5	AAY99873
5	2003	98.6	398	8	ADM82878
6	2003	98.6	418	1	AAP40133
7	2003	98.6	418	1	AAP94664
8	2003	98.6	418	2	AAY26925
9	2003	98.6	418	5	ABG96414
10	2003	98.6	418	6	ABR55849
11	2003	98.6	418	7	ADB99858
12	2003	98.6	418	7	ADG63536
13	2003	98.6	418	7	ADG63532
14	2003	98.6	418	7	ADG63532
15	2003	98.6	418	7	ADG63532
16	2003	98.6	418	7	ADG63532
17	2003	98.6	418	8	ADG25246
18	2003	98.6	418	8	ADNA9694
19	2003	98.6	418	8	ADM82877
20	2003	98.6	503	5	AAY99884
21	2003	98.6	503	5	AAY99881
22	2003	98.6	522	5	AAY99883
23	2003	98.6	522	5	AAY99885
24	2003	98.6	580	5	AAY99882
25	2003	98.6	580	5	AAY99889

99 1311 64.5 418 7 ADE08102 Novel pro
100 1301 64.0 413 2 AAW23649 Recombina

ALIGNMENTS

RESULT 1
AA44201

ID AAY44201 standard; protein; 394 AA.

XX AC AAY44201;

XX DT 25-JAN-2000 (first entry)

XX DE Alpha-1 antitrypsin variant Portland.

XX KW Alpha-1 antitrypsin variant Portland; alpha-1 antitrypsin; PDX;
KW protease inhibitor; furin endoprotease; peptide mimetic; bacterial toxin;
KW furin recognition site; portland protein; SYBYL program; pharmacophore;
KW protein crystal structure analysis; reactive site loop; RSL;
KW endolytic maturation; endoproteolytic activation; Pseudomonas aeruginosa;
KW Corynebacterium diptheriae; Bacillus anthracis; cytomegalovirus;
KW biologically active protein.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 355

FT /note= "Wild type Ala substituted by Arg"

FT Misc-difference 358

FT /note= "Wild type Met substituted by Arg"

XX PN WO9951624-A1.

XX XX 14-OCT-1999.

XX PF 08-APR-1999; 99WO-US007776.

XX PR 08-APR-1998; 98US-0081034P.

XX PA (UYOR-) UNIV OREGON HEALTH SCI.

XX PI Jean F, Thomas G;

XX XX WPI; 1999-620190/53.

XX DR New furin endoprotease inhibitor that mimics a specific region of alphas-
PT antitrypsin Portland mutant, for treatment and prevention of bacterial
PT and viral infection.

XX PS Claim 1; Page 98-99; 108pp; English.

XX CC The present sequence is alpha-1 antitrypsin mutated variant Portland
CC (also termed PDX). This effectively inhibits furin endoprotease. Peptides
CC or peptide mimetics derived from this sequence inhibit bacterial toxins
CC that are processed at a consensus furin recognition site, when
CC administered in therapeutically effective amounts. Portland protein
CC generated by the SYBYL program and the crystal structure analysed for
CC designing the pharmacophore for the reactive site loop of the Portland
CC variant. Endoproteolytic activation of bacterial toxins and endolytic
CC maturation of viral proteins is blocked by the peptide and peptide
CC mimetics. This is useful in treating infections of cells by bacteria
CC (specifically Corynebacterium diptheriae, Bacillus anthracis and
CC Pseudomonas aeruginosa) or viruses (specifically cytomegalovirus). It may
CC also be used to inhibit processing of biologically active proteins

XX SQ Sequence 394 AA;

Query Match

Best Local Similarity 100.0%; Score 2032; DB 2; Length 394;

Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDPOGAAQKTDTSDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB |||||
1 EDPOGAAQKTDTSDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
QY 61 FAMLSTGKADTHDEILGLNPNLTQIPEAQIHGFGQELLRTLNQPSQLQTTGNGLFL 120
DB |||||
61 FAMLSTGKADTHDEILGLNPNLTQIPEAQIHGFGQELLRTLNQPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFLEDKVKKLYHSEAFVNFQGTQAKKOINDYVEKGTQGIKIVDLVKELDRDT 180
DB |||||
121 SQGLKLVDFLEDKVKKLYHSEAFVNFQGTQAKKOINDYVEKGTQGIKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKGGKWERPEVKDTEDEDFHVDQVTVKVPMMKRLGFNIQHCKLSSWVL 240
DB |||||
181 VFALVNYIFFKGGKWERPEVKDTEDEDFHVDQVTVKVPMMKRLGFNIQHCKLSSWVL 240
QY 241 LMKYLGNAITAFFLPDEGKLOHLENELTHDITKPLENEDRRRSASLHLPKLSITGTYDLK 300
DB |||||
241 LMKYLGNAITAFFLPDEGKLOHLENELTHDITKPLENEDRRRSASLHLPKLSITGTYDLK 300
QY 301 SVLGOLGITKTVFSNGADLSGVTEERAPLKSVAHVKAULTIDEKGTAAAGAMFLERIPRSI 360
DB |||||
301 SVLGOLGITKTVFSNGADLSGVTEERAPLKSVAHVKAULTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVNPVPTGK 394
DB |||||
361 PPEVKFNKPFVFLMIEQNTKSPLEFMGKVNPVPTGK 394

RESULT 2

AA44205

ID AAY44205 standard; protein; 394 AA.

XX AC AAY44205;

XX DT 25-JAN-2000 (first entry)

XX DE Alpha-1 antitrypsin variant Pittsburgh.

XX KW Alpha-1 antitrypsin variant Pittsburgh; alpha-1 antitrypsin; PIT;
KW negative control; furin inhibition assay; peptide mimetic; A7 cell;
KW Pseudomonas aeruginosa exotoxin A; PEA; HCMV glycoprotein gB.

XX OS Synthetic.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Misc-difference 358

FT /note= "Wild type Met substituted by Arg"

XX PN WO9951624-A1.

XX XX 14-OCT-1999.

XX PF 08-APR-1999; 99WO-US007776.

XX PR 08-APR-1998; 98US-0081034P.

XX XX (UYOR-) UNIV OREGON HEALTH SCI.

XX PI Jean F, Thomas G;

XX WPI; 1999-620190/53.

XX DR New furin endoprotease inhibitor that mimics a specific region of alphas-
PT antitrypsin Portland mutant, for treatment and prevention of bacterial
PT and viral infection.

XX PS Example 1; Page 101-102; 108pp; English.

XX CC The present sequence is alpha-1 antitrypsin mutated variant Pittsburgh
CC (also termed PIT). PIT protein was used as a negative control in furin

CC inhibition assay to assess the biological activity of the peptide
CC mimetics. A7 cells when incubated with PIR exhibited little or no
CC protective effect in the presence of Pseudomonas aeruginosa exotoxin A.
CC PIR was also used as a negative control for the assay to detect PDX -
CC mediated inhibition of furin-catalysed maturation of HCMV glycoprotein gB
XX
XX Sequence 394 AA;
SQ

Query Match 99.7%; Score 2026; DB 2; Length 394;
Best Local Similarity 99.7%; Pred. No. 1.7e-157;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
DB 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
QY 61 FAMLISLGTAKADTHDEILEGLNPNLTQIPAEQIHGEFQELLRLTNQDPSQLQTTGNGLFL 120
DB 61 FAMLISLGTAKADTHDEILEGLNPNLTQIPAEQIHGEFQELLRLTNQDPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFLEDDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQKIVDLVKELDRDT 180
DB 121 SQGLKLVDFLEDDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKQKWERPFVKTDEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 240
DB 181 VFALVNYIFFKQKWERPFVKTDEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 240
QY 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDDRSASLHLPKLSITGYDLK 300
DB 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDDRSASLHLPKLSITGYDLK 300
QY 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 3
AAW59839
ID AAW59839 standard; protein; 394 AA.
AC AAW59839;
XX
DT 20-NOV-1998 (first entry)
XX
DE Mature protein sequence of alphas-1-antitrypsin (AAT).
XX
KW Protein expression; monocotyledon plant cell;
KW glycosylated alpha 1-antitrypsin; AAT; glycosylated antithrombin III;
KW Atrial; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema;
KW antithrombotic; blood replacement.
XX
OS Homo sapiens.
XX
XX WO9836085-A1.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-US003068.
XX
PR 13-FEB-1997; 97US-0037991P.
PR 13-FEB-1997; 97US-0038168P.
PR 13-FEB-1997; 97US-0038169P.
PR 13-FEB-1997; 97US-0038170P.
XX
XX (PHYT-) APPLIED PHYTOLOGICS INC.
XX
XX Sutliff TD, Rodriguez RL;
XX

DR WPI; 1998-467179/40.
DR N-PSDB; AAV411726.
XX
XX Expressing mature, glycosylated proteins in monocotyledonous plant cells
PT - from chimeric gene including signal peptide sequence, specifically
PT therapeutic agents and industrial enzymes.
XX
XX Disclosure; Page 28-29; 53pp; English.
XX
XX The present sequence represents the mature protein of alpha-1-antitrypsin
CC (AAT). The protein is used to exemplify the invention. The specification
CC describes a method for producing mature heterologous protein in
CC monocotyledonous plant cells. The method comprises transforming the cells
CC with a chimeric gene comprising a monocotyledon transcription regulator,
CC inducible either during seed maturation or by adding/removing a small
CC molecule, DNA encoding the heterologous protein, and DNA encoding a
CC signal peptide, with the signal peptide causing secretion of the protein
CC from the cell. Proteins expressed in this manner include mature
CC glycosylated alpha 1-antitrypsin (AAT) with a glycosylation pattern that
CC significantly increases its serum half-life, mature glycosylated
CC antithrombin III (ATIII), mature human serum albumin (HSA) having the
CC native folding pattern as shown by bilirubin-binding characteristics, or
CC mature active subtilisin BPN'. These proteins are useful therapeutically
CC (e.g. AAT for treating emphysema, ATIII as antithrombotic and HSA as
CC blood replacement) or as industrial enzymes (BPN' is used in detergents)
XX
XX Sequence 394 AA;
SQ

Query Match 98.6%; Score 2003; DB 2; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.3e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
DB 1 EDPOGDAQAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
QY 61 FAMLISLGTAKADTHDEILEGLNPNLTQIPAEQIHGEFQELLRLTNQDPSQLQTTGNGLFL 120
DB 61 FAMLISLGTAKADTHDEILEGLNPNLTQIPAEQIHGEFQELLRLTNQDPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFLEDDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQKIVDLVKELDRDT 180
DB 121 SQGLKLVDFLEDDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKQKWERPFVKTDEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 240
DB 181 VFALVNYIFFKQKWERPFVKTDEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 240
QY 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDDRSASLHLPKLSITGYDLK 300
DB 241 LMKYLGNAATAIFFLPDEGKLOHLENELTHDIITKFLNEDDRSASLHLPKLSITGYDLK 300
QY 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 4
AAU99873
ID AAU99873 standard; protein; 394 AA.
XX
AC AAU99873;
XX
DT 07-OCT-2002 (first entry)
XX
DE Human alpha-1-antitrypsin (AAT) protein.
XX
KW Alpha-1-antitrypsin; AAT; human; protease inhibitor; malaria; emphysema;
KW asthma; chronic obstructive pulmonary disease; eczema; cystic fibrosis;
XX

KW otitis media; otitis external; HIV; psoriasis;
KW human immunodeficiency virus; atopic dermatitis; muscular dystrophy;
KW herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease;
KW tumour metastasis; tumour angiogenesis; osteoporosis; Paget's disease;
KW glomerulonephritis; scleroderma; Alzheimer's disease; hypertension.
XX Homo sapiens.
XX WO200250287-A2.
XX PD 27-JUN-2002.
XX PF 18-DEC-2001; 2001WO-US049256.
XX PR 18-DEC-2000; 2000US-0256699P.
XX PR 20-NOV-2001; 2001US-0331962P.
XX PA (ARRI-) ARRIVA PHARM INC.
XX PI Barr PJ, Gibson HL, Pemberton P;
XX WPI; 2002-500631/53.
XX DR N-PSDB; ABK88015.
XX Novel fusion protein useful for inhibiting protease activity associated
PT with a disorder such as emphysema, asthma, comprises a first protease
PT inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor.
XX Claim 25; Page 25-27; 134pp; English.
XX This invention relates to a novel fusion protein comprising a first
CC protease inhibitor comprising an alpha1-antitrypsin or its functionally
CC active portion and a second protease inhibitor or its functionally active
CC protein. The fusion proteins of the invention may act as an inhibitor of
CC protease activity. The fusion protein of the invention is useful for
CC inhibiting protease activity associated with a disorder such as
CC emphysema, asthma, chronic obstructive pulmonary disease, cystic
CC fibrosis, otitis media, otitis external or HIV infection, or for treating
CC an individual suffering from or at risk for a disease or disorder
CC involving unwanted protease activity. The proteins are useful for
CC treating dermatological diseases such as atopic dermatitis, eczema and
CC psoriasis, in inflammatory responses to viral infection, and for treating
CC herpes infection, corneal or epidermal ulceration, chronic non-healing
CC wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour
CC metastasis and tumour angiogenesis, gastric ulceration, osteoporosis,
CC Paget's disease, glomerulonephritis, scleroderma, malaria, bacterial
CC infection, Alzheimer's disease, hypertension and muscular dystrophy. The
CC present sequence represents the human alpha-1-antitrypsin (AAT) protein
CC used to create the fusion protein of the invention
XX
XX Sequence 394 AA;
Query Match 98.6%; Score 2003; DB 5; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.3e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQKTTSHHDDPHFNKITNLAEFAFSLYRQLAQHSNSTNIPSPVSIATA 60
DB 1 EDPOGDAQKTTSHHDDPHFNKITNLAEFAFSLYRQLAQHSNSTNIPSPVSIATA 60
QY 61 FAMLISGKTADTHDEILEGLNENLTIQIPRAQIHGFGFQELLRTLNQPSQLQTTGNGLFL 120
DB 61 FAMLISGKTADTHDEILEGLNENLTIQIPRAQIHGFGFQELLRTLNQPSQLQTTGNGLFL 120
QY 121 SGGLKLVKFLBVDVKVLHSEAFNTNFGTEQAQKQINDYVEKGTQGGKIVDLVKELDRPT 180
DB 121 SGGLKLVKFLBVDVKVLHSEAFNTNFGTEQAQKQINDYVEKGTQGGKIVDLVKELDRPT 180
QY 181 VFALVNYLFFKCKRPERPEVKDTEDEDFHVDQVTVTKVPMKRLGWNIOHCCKLSSWVL 240
DB 181 VFALVNYLFFKCKRPERPEVKDTEDEDFHVDQVTVTKVPMKRLGWNIOHCCKLSSWVL 240
QY 241 LMKYLGNATAIFFLPDEGKLQHLENLTHDITTKFLENERRSASLHLPKLSITGTYDLK 300

DB 241 LMKYLGNATAIFFLPDEGKLQHLENLTHDITTKFLENERRSASLHLPKLSITGTYDLK 300
QY 301 SVLGQLGTTKTVFSNGADLSGVTTEAPLKLKAVHKAIVLTIDEKGTAAAGAMFLEIPRSI 360
DB 301 SVLGQLGTTKTVFSNGADLSGVTTEAPLKLKAVHKAIVLTIDEKGTAAAGAMFLEIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLPMGKVNNPTGK 394
DB 361 PPEVKFNKPFVFLMIEQNTKSPFLPMGKVNNPTGK 394
RESULT 5
ADM82878
ID ADM82878 standard; protein; 398 AA.
XX AC ADM82878;
XX DT 29-JUL-2004 (first entry)
XX DE Mouse alpha-1-antitrypsin (AAT) mature protein SEQ ID NO:4.
XX KW alpha 1-antichymotrypsin; ACT; alpha 1-antitrypsin; AAT; gene therapy;
KW protein therapy; diabetic ulcer; arterial ulcer; ulcus cruris arteriosum;
KW necrobiosis lipoidica; ulcera arteriosa; wound healing; human.
XX OS Homo sapiens.
XX FN EP1415664-A1.
XX PD 06-MAY-2004.
XX PF 30-OCT-2002; 2002EP-00024200.
XX PR 30-OCT-2002; 2002EP-00024200.
XX PA (SWIT-) SWITCH BIOTECH AG.
XX PI Halle J, Goppelt A;
XX WPI; 2004-341870/32.
XX DR N-PSDB; ADM82879.
XX PT Use of alpha 1-antichymotrypsin polypeptide in combination with alpha 1-
PT antitrypsin polypeptide for treating and/or preventing poorly healing
PT diabetes-associated and/or poorly healing arterial wounds e.g., diabetic
PT ulcer.
XX Claim 2; SEQ ID NO 4; 31pp; English.
XX The present invention describes a method of using alpha 1-
XX antichymotrypsin (ACT), its functional variant and/or encoding nucleic
XX acid, or of a cell expressing ACT polypeptide or its encoding nucleic
XX acid, in combination with alpha 1-antitrypsin (AAT), its functional
XX variant or encoding nucleic acid, or with a cell expressing AAT
XX polypeptide or its encoding nucleic acid, for treating and/or preventing
XX poorly healing diabetes-associated and/or arterial wounds. Also described
XX is a method of manufacturing a pharmaceutical composition for treating
XX and/or preventing the diseases, where the ACT polypeptide or its encoding
XX nucleic acid or a cell expressing the ACT polypeptide or its encoding
XX nucleic acid is combined with the AAT polypeptide or its encoding nucleic
XX acid or a cell expressing the AAT polypeptide or its encoding nucleic
XX acid. ACT and AAT can be used in gene and protein therapy. The ACT and
XX AAT polypeptides (in combination) are useful for treating and/or
XX preventing poorly healing diabetes-associated and/or poorly healing
XX arterial wounds such as diabetic ulcer and arterial ulcer, preferably
XX diabetic ulcer. Diabetic ulcers are skin lesions in mammals and humans
XX suffering from diabetes (e.g., include ulcus cruris arteriosum,
XX necrobiosis lipoidica and ulcera arteriosa) and delayed wound healing is
XX caused by arteriosclerotic destruction of the blood vessels. The present
XX sequence represents the mature human AAT, which is used in the
XX exemplification of the present invention.

```

SQ      Sequence 398 AA;
Query Match      98.6%; Score 2003; DB 8; Length 398;
Best Local Similarity 98.5%; Pred. No. 1.3e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EDPOGDAQAQKTDSHHDDQHPFNKITPNLAFSAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB      5 EDPOGDAQAQKTDSHHDDQHPFNKITPNLAFSAFSLYRQLAHQSNSTNIFPSPVSIATA 64
QY      61 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB      65 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 124
QY      121 SOGLKLVDFLEDKVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB      125 SBGLKLVDFLEDKVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 184
QY      181 VFALVNYIIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKKLSWWYL 240
DB      185 VFALVNYIIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKKLSWWYL 244
QY      241 LMKYLGNAATAIFLPDEGKLOHLENELTHDITTKPLENEDRRSASLHLPKLSITGYDLK 300
DB      245 LMKYLGNAATAIFLPDEGKLOHLENELTHDITTKPLENEDRRSASLHLPKLSITGYDLK 304
QY      301 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDEGTEAAGAMFLERIPRSI 360
DB      305 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDEGTEAAGAMFLERIPRSI 364
QY      361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB      365 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 398

RESULT 6
AAP40133
ID      AAP40133 standard; protein; 418 AA.
XX
AC      AAP40133;
XX
DT      25-MAR-2003 (revised)
DT      16-FEB-1992 (first entry)
XX
XX      Sequence of human alpha-1-antitrypsin.
DE      Protease inhibitor; enzyme; proteolysis inhibitor; emphysema; therapy.
KW      Homo sapiens.
OS
FH      Key      Location/Qualifiers
FT      Peptide 1..24
FT      Region 25..418
XX
XX      EP103409-A.
PN
XX
XX      21-MAR-1984.
PD
XX
XX      12-AUG-1983; 83EP-00304668.
PF
XX
XX      13-AUG-1982; 82US-00408099.
PR
XX      13-AUG-1982; 88EP-00201179.
PR
XX      18-AUG-1982; 82US-00409183.
PR
XX      28-APR-1983; 83US-00489406.
XX
XX      (ZYMO-) ZYMOS CORP.
PA      (BGM ) BRIGHAM & WOMENS HOSPITAL.
PA      (KAWA/) KAWASAKI G H.
XX
XX      Kawasaki GH, Woodbury RG;
XX
XX      WPI; 1984-077108/13.
DR

DR      N-PSDB; AAM40078.
XX
XX      Extra:chromosomal element for replication in yeast - with yeast promoter
PT      for regulation of glycolytic protein prodn.
XX
XX      Disclosure; Fig 1A; 48pp; English.
PS
XX
XX      The inventors claim a DNA construct contg. a gene encoding human alpha-1-
CC      antitrypsin. A substantially pure, substantially unglycosylated mammalian
CC      alpha-1-antitrypsin is also claimed. (Updated on 25-MAR-2003 to correct
CC      PA field.)
XX
XX      Sequence 418 AA;
SQ

Query Match      98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 EDPOGDAQAQKTDSHHDDQHPFNKITPNLAFSAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB      25 EDPOGDAQAQKTDSHHDDQHPFNKITPNLAFSAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY      61 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB      85 FAMLISLGTAKADTHDEILEGLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY      121 SOGLKLVDFLEDKVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB      145 SBGLKLVDFLEDKVKKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY      181 VFALVNYIIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKKLSWWYL 240
DB      205 VFALVNYIIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKKLSWWYL 264
QY      241 LMKYLGNAATAIFLPDEGKLOHLENELTHDITTKPLENEDRRSASLHLPKLSITGYDLK 300
DB      265 LMKYLGNAATAIFLPDEGKLOHLENELTHDITTKPLENEDRRSASLHLPKLSITGYDLK 324
QY      301 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDEGTEAAGAMFLERIPRSI 360
DB      325 SVLGQGITKVFNSGADLSGVTEEAPLKLKSAVHKAVLTIDEGTEAAGAMFLERIPRSI 384
QY      361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB      385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 7
AAP94664
ID      AAP94664 standard; protein; 418 AA.
XX
AC      AAP94664;
XX
DT      25-MAR-2003 (revised)
DT      28-JUN-1990 (first entry)
XX
XX      Predominant form of human alpha-1-antitrypsin as encoded by cDNA.
DE
KW      Human alpha-1-tryptsin (hAT); anti-A1 antibodies; proteolytic activity;
KW      AT deficiency; Saccharomyces cerevisiae GK100; 2-mu plasmid DNA; CATI;
KW      Plasmid HAT4; yeast TPI promoter; yeast TPI terminator; plasmid Cl/L.
XX
XX      Homo sapiens.
OS
FH      Key      Location/Qualifiers
FT      Peptide 1..118
FT      Protein 119..418
XX
XX      EP304971-A.
PN
XX
XX      01-MAR-1989.
PD
XX
XX      12-AUG-1983; 88EP-00201179.
PF

```

XX 13-AUG-1982; 82US-00408099.
PR 28-APR-1983; 83US-00489406.
XX (ZYMO) ZYMOGENETICS INC.
XX Kawasaki GH, Woodbury RG;
PI
XX WPI: 1989-062651/09.
DR N-PSDB; AAN91077.
XX New alpha-1-antitrypsin polypeptide(s) - produced by recombinant DNA
PT techniques, esp. using yeast host.
PT
XX Disclosure; Page ?; 28pp; English.
XX
CC New in the patent are unglycosylated polypeptides having the amino acid
CC sequence of a mammalian alpha-1-antitrypsin (AT). Also claimed is the
CC prodn. of polypeptides having the protease-inhibiting activity of a
CC mammalian AT. A culture of microorganisms is grown such as fungi or
CC yeast, esp. Saccharomyces cerevisiae GK 100, which are transformed with a
CC DNA transfer vector 2-mu plasmid, plasmid CATI or plasmid HAT4, contg. a
CC segment encoding the mammalian AT. The unglycosylated polypeptides are
CC useful for prodn. of anti-AT antibodies, for modulating proteolytic
CC activity in mammals, and for treating AT deficiency, esp. for replacing
CC AT which has been inactivated (oxidised) by tobacco or other smoke. In
CC the given example plasmid HAT4 comprises the yeast promoter, an
CC ATGAGGATCC adapter, the HAT gene and the yeast TPI terminator inserted
CC into plasmid CI/1, which contains the entire 2-mu DNA from S. cerevisiae.
CC S. cerevisiae GK100 transformed with HAT4 produces soluble protein with
CC an HAT content of 2-3% when grown on a medium contg. 6% glucose. (Updated
CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC PR field.)
XX
SQ Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGTKADTHDELEGNLNLTOIPEAQIHEGFQELLRTLNQDPSQLOLTTGNGLFL 120
DB 85 FAMLISGTKADTHDELEGNLNLTOIPEAQIHEGFQELLRTLNQDPSQLOLTTGNGLFL 144
QY 121 SQGLKLVDFLEDDVKKLYHSEAFVNFQDTEQAKQINDYVEKGQKIVDVLVKELDRDT 180
DB 145 SGLKLVDFLEDDVKKLYHSEAFVNFQDTEQAKQINDYVEKGQKIVDVLVKELDRDT 204
QY 181 VFALVNYIFFKQKWERPFVKDTEBEDFHDVQVTVTKVPMKRLGMFNIOHCKKLSWWVL 240
DB 205 VFALVNYIFFKQKWERPFVKDTEBEDFHDVQVTVTKVPMKRLGMFNIOHCKKLSWWVL 264
QY 241 LMKYLGNAITAFPLPDEGKQHLNELTHDIIITKFLNEDRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKQHLNELTHDIIITKFLNEDRSASLHLPKLSITGYDLK 324
QY 301 SVLGQLGITKVFNSGADLSGVTEEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQLGITKVFNSGADLSGVTEEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 8
AAY26925
ID AAY26925 standard; protein; 418 AA.
XX

AC AAY26925;
XX 21-DEC-1999 (first entry)
XX
DE Human alaph-anti-trypsin type M1 protein.
XX
KW Human; alaph-1-anti-trypsin; transgenic plant; monocotyledon; variant;
KW glycosylation; serine protease; inhibitor; neutrophil; elastase; trypsin;
KW cathepsin G; thrombin; pulmonary tissue; protease damage; septic shock;
KW pulmonary emphysema; cystic fibrosis; rheumatism; recombinant;
KW virus contamination; immunogenicity; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..24
FT /label= signal_peptide
FT Protein 25..418
FT /label= mature protein
FT Modified-site 70
FT /note= "putative glycosylation site"
FT Modified-site 107
FT Modified-site 271
FT Active-site 382..387
FT /note= "putative active site"
XX
PN W09938987-A1.
XX
XX 05-AUG-1999.
PD
XX 29-JAN-1999; 99WO-FR000195.
PF
XX 30-JAN-1998; 98FR-00001089.
PR
XX (MERI-) MERISTEM THERAPEUTICS.
PA
XX Gruber V, Olganier B, Bournat P, Theisen M, Merot B;
PI
XX WPI: 1999-469334/39.
DR N-PSDB; AAX83548.
XX
PT Production of alaph-antitrypsin, and its variants, in cells of
PT monocotyledonous plants, useful as serine protease inhibitors for
PT therapy, e.g. of emphysema, in cosmetics and as reagents.
PS
PS Claim 8; Fig 1; 67pp; French.
XX
CC This sequence represents the coding region of the human alpha-1-anti-
CC trypsin (AT) gene. The invention relates to the production of AT in plant
CC cells, especially monocotyledonous plants. Also produced are variants of
CC the AT protein, in which the glycosylation pattern of the protein is
CC altered. AT inhibits serine proteases, specifically neutrophil elastase
CC (but also trypsin, cathepsin G, thrombin etc.) so protect pulmonary
CC tissue against protease damage. AT are used to treat AT-deficiency
CC conditions, particularly pulmonary emphysema, cystic fibrosis, septic
CC shock and rheumatism. The use of plants for the recombinant production of
CC AT results in a product without risk of (sub)viral contamination. The
CC recombinant AT had good activity and is stable, with low immunogenicity
CC (associated with glycosylation patterns similar to the native protein)
XX
SQ Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 2; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPQGDAAQKTDTSHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGTKADTHDELEGNLNLTOIPEAQIHEGFQELLRTLNQDPSQLOLTTGNGLFL 120
DB 85 FAMLISGTKADTHDELEGNLNLTOIPEAQIHEGFQELLRTLNQDPSQLOLTTGNGLFL 144

QY 1 EDPOGDAQAQKTDTSHHDQDPTFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDQDPTFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLSTGTTKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGTTKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SQGLKLVDPLEVDKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGKLVDPLEVDKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VPALVNYIYFFKQWEPFVKDTEEDFHVQDVTTVKVPMMKGLGMFNTOHCKKLSWVL 240
DB 205 VPALVNYIYFFKQWEPFVKDTEEDFHVQDVTTVKVPMMKGLGMFNTOHCKKLSWVL 264
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQGITKTVFSNGADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKTVFSNGADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIRONTKSPFLFMGKVVNPTQK 394
DB 385 PPEVKFNKPFVFLMIRONTKSPFLFMGKVVNPTQK 418

RESULT 12

ADE63536
ID ADE63536 standard; protein; 418 AA.

AC ADE63536;

DT 29-JAN-2004 (first entry)

DE Human Protein P01009, SEQ ID NO 9480.

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GENE) GEN HOSPITAL CORP.

PA (FAH) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P01009.

XX New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 7; Length 418;

Best Local Similarity 98.5%; Pred. No. 1.4e-155;

Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDQDPTFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60

DB 25 EDPOGDAQAQKTDTSHHDQDPTFNKTPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 84

QY 61 FAMLSTGTTKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 120

DB 85 FAMLSTGTTKADTHDEILEGLNPNLTQIPRAQIHGEGFQELLRTLNQDPSQLQTTGNGLFL 144

QY 121 SQGLKLVDPLEVDKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180

DB 145 SEGKLVDPLEVDKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VPALVNYIYFFKQWEPFVKDTEEDFHVQDVTTVKVPMMKGLGMFNTOHCKKLSWVL 240

DB 205 VPALVNYIYFFKQWEPFVKDTEEDFHVQDVTTVKVPMMKGLGMFNTOHCKKLSWVL 264

QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 300

DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTGYDLK 324

QY 301 SVLGQGITKTVFSNGADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360

DB 325 SVLGQGITKTVFSNGADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIRONTKSPFLFMGKVVNPTQK 394

DB 385 PPEVKFNKPFVFLMIRONTKSPFLFMGKVVNPTQK 418

RESULT 13

ADE63528

ID ADE63528 standard; protein; 418 AA.

XX ADE63528;

XX 29-JAN-2004 (first entry)

DE Human Protein P01009, SEQ ID NO 9472.

XX Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX

modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 7; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAQHSNSTNIPFSPVSIATA 60
DB 25 EDPQGDAAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAQHSNSTNIPFSPVSIATA 84
QY 61 FAMLISLGTAKADTHDEILGELNPNLQIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAMLISLGTAKADTHDEILGELNPNLQIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 144
QY 121 SQGLKLVKFLDVKLVKLYHSEAFVNFQDTEAKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVKFLDVKLVKLYHSEAFVNFQDTEAKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKQWERPPEVKDTEEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSWWYL 240
DB 205 VFALVNYIFFKQWERPPEVKDTEEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSWWYL 264
QY 241 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDITITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDITITKPLENEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGOLGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDKGTGAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDKGTGAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGVKNVPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGVKNVPTGK 418

RESULT 15
ADE63524
ID ADE63524 standard; protein; 418 AA.
XX ADE63524;
XX
XX
XX 29-JAN-2004 (first entry)
XX Human Protein P01009, SEQ ID NO 9468.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX

PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P01009.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 418 AA;

Query Match 98.6%; Score 2003; DB 7; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAQHSNSTNIPFSPVSIATA 60
DB 25 EDPQGDAAQKTDTSHHDDQDHPFNKIPNLAEFAFSLYRQLAQHSNSTNIPFSPVSIATA 84
QY 61 FAMLISLGTAKADTHDEILGELNPNLQIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAMLISLGTAKADTHDEILGELNPNLQIPEAQIHGEGFQELLRTLNQPSQLQTTGNGLFL 144
QY 121 SQGLKLVKFLDVKLVKLYHSEAFVNFQDTEAKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVKFLDVKLVKLYHSEAFVNFQDTEAKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKQWERPPEVKDTEEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSWWYL 240
DB 205 VFALVNYIFFKQWERPPEVKDTEEDFHVQDVTTVKVPMMKRLGNFNIQHCKLSWWYL 264
QY 241 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDITITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDITITKPLENEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGOLGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDKGTGAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGADLSGVTEEPAPLKLKSAVKHKAULTIDKGTGAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGVKNVPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGVKNVPTGK 418

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Job time : 80 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:40:45 ; Search time 43 Seconds
(without alignments)
683.994 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPOGDAAQKDTSHHDQH.....IEQNTKSPLEMGKVNPTGK 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2032	100.0	394	3	US-08-481-534-9
2	2026	99.7	394	3	US-08-481-534-11
3	2021	99.5	394	1	US-08-002-202-9
4	2020	99.4	394	3	US-08-481-534-6
5	2015	99.2	394	1	US-08-002-202-11
6	2009	98.9	394	1	US-08-002-202-6
7	2003	98.6	394	3	US-09-023-339-1
8	2003	98.6	418	1	US-08-121-714-3
9	2003	98.6	418	1	US-08-477-1182-3
10	2003	98.6	418	2	US-08-477-1182-3
11	2003	98.6	418	4	US-10-030-330-3
12	2003	98.6	418	5	PCT-US93-08322-3
13	1993	98.1	418	4	US-10-000-489-92
14	1992	98.0	394	2	US-08-553-488A-1
15	1973	97.1	414	1	US-08-002-202-19
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18	1967	96.8	414	3	US-08-481-534-13
19	1961	96.5	414	1	US-08-002-202-17
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21	1714	84.4	363	4	US-09-755-665-58
22	1665.5	82.0	351	4	US-10-000-489-50
23	1371	67.5	308	1	US-07-859-480-2
24	1157.5	57.0	421	4	US-09-949-016-8165
25	1125	55.4	420	4	US-09-949-016-6705
26	833	41.0	423	4	US-09-976-594-19
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30	811.5	39.9	405	1	US-07-994-423-2	Sequence 2, Appli
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33	804	39.6	422	4	US-09-244-111-8	Sequence 8, Appli
34	791	38.9	414	4	US-09-755-665-14	Sequence 14, Appli
35	791	38.9	414	4	US-09-755-665-55	Sequence 55, Appli
36	791	38.9	414	4	US-09-755-665-56	Sequence 56, Appli
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43	752.5	37.0	435	4	US-09-512-628-5	Sequence 5, Appli
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46	541.5	26.6	444	3	US-09-271-608-8	Sequence 8, Appli
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53	522.5	25.7	390	3	US-09-266-910-4	Sequence 4, Appli
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60	494.5	24.3	382	1	US-07-768-286B-6	Sequence 6, Appli
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66	487	24.0	415	3	US-09-026-408-4	Sequence 4, Appli
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68	481	23.7	415	1	US-07-911-531-19	Sequence 19, Appli
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80	475.5	23.4	374	1	US-08-846-784-2	Sequence 2, Appli
81	475.5	23.4	386	4	US-08-543-573A-39	Sequence 39, Appli
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ALIGNMENTS

RESULT 1
US-08-481-534-9
; Sequence 9, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 355..358 /label=Variant
; OTHER INFORMATION: / note="The amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: protein, alpha-1-antitrypsin Portland."

US-08-481-534-9
Query Match 100.0%; Score 2032; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 6.4e-184;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNNPTGK 394

RESULT 2
US-08-481-534-11
; Sequence 11, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6022855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified site
; LOCATION: 355..358 /label=Variant
; OTHER INFORMATION: / note="The amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: protein, alpha-1-antitrypsin Pittsburgh."

Query Match 99.7%; Score 2026; DB 3; Length 394;
Best Local Similarity 99.7%; Pred. No. 2.4e-183;

Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 361 PPEVKFNKPFVFLMTEQNTKSPFLFMGKVNPPTGK 394

RESULT 3

US-08-002-202-9
; Sequence 9, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Allegratti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..394
; OTHER INFORMATION: /label= Variant
; OTHER INFORMATION: /note= "This amino acid sequence is the amino acid
; sequence of the modified alpha-1-antitrypsin
; protein, alpha-1-antitrypsin Portland;"
US-08-002-202-9
Query Match 99.5%; Score 2021; DB 1; Length 394;
Best Local Similarity 99.5%; Pred. No. 7,1e-183;
Matches 392; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
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DB 61 FAWLSIGTKADTHDEILEGLNPNLQIPEAQIHEGFQELLRLTNQDPSQLQTTGNGLFL 120
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DB 181 VPALVNYIFFKGKWRPFVKDTEBEDFHVQDQVTVKVPMMKRLGMFNTOHCKKLSWWYL 240
QY 241 LMKYLGNTATFPLPDEGKLOHLENELTHDIIITKLENEEDRESASLHLPKLSITGYDILK 300
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RESULT 4

US-08-481-534-6
; Sequence 6, Application US/08481534
; Patent No. 6022855
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,534
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:

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; NAME: No. 602855nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-481-534-6

Query Match 99.4%; Score 2020; DB 3; Length 394;
Best Local Similarity 99.5%; Pred. No. 8.8e-183;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 241 LMKYLGNAATAIFFLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDILK 300
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QY 301 SVLGQGITKVFSGNADLSGVTEEAAPLKLKAVHKAVLTIDKGTGAAGMFLERIPRSI 360
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RESULT 5
US-08-002-202-11
; Sequence 11, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1-394
; OTHER INFORMATION: /label= Variants
; OTHER INFORMATION: /note= "This amino acid sequence is the amino acid
; OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin
; OTHER INFORMATION: variant, alpha-1-antitrypsin Pittsburgh "
US-08-002-202-11

Query Match 99.2%; Score 2015; DB 1; Length 394;
Best Local Similarity 99.2%; Pred. No. 2.6e-182;
Matches 391; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPOGDAQAQKDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
QY 61 FAMLISLGTAKADTHDEILEGLNPNLQIPEAQIHEGFQELLRLTNQPSQLQTLTTGNGLFL 120
Db 61 FAMLISLGTAKADTHDEILEGLNPNLQIPEAQIHEGFQELLRLTNQPSQLQTLTTGNGLFL 120
QY 121 SOGLKLVKFLKEDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVLVKELDRDT 180
Db 121 SOGLKLVKFLKEDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVLVKELDRDT 180
QY 181 VFALVNYIFFKQKWRPFVVKDTEEDFHVDQVTVTKVPMKRLGMFNIQHCKLSSWVL 240
Db 181 VFALVNYIFFKQKWRPFVVKDTEEDFHVDQVTVTKVPMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNAATAIFFLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDILK 300
Db 241 LMKYLGNAATAIFFLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDILK 300
QY 301 SVLGQGITKVFSGNADLSGVTEEAAPLKLKAVHKAVLTIDKGTGAAGMFLERIPRSI 360
Db 301 SVLGQGITKVFSGNADLSGVTEEAAPLKLKAVHKAVLTIDKGTGAAGMFLERIPRSI 360
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 6
US-08-002-202-6
; Sequence 6, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Furin Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.

```

STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-002-202-6

Query Match 98.9%; Score 2009; DB 1; Length 394;
Best Local Similarity 99.0%; Pred. No. 9.7e-182;
Matches 390; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNFFSPVSIATA 60
DB 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNFFSPVSIATA 60
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRLTNQPSQLQTTGNGFL 120
DB 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRLTNQPSQLQTTGNGFL 120
QY 121 SOGLKLVDFLEDKVKKLYHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 121 SOGLKLVDFLEDKVKKLYHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKGKWRPFVKDTEEDFHVDOVTVKVPMMKRLGMFNIQHCKLSSWVL 240
DB 181 VFALVNYIFFKGKWRPFVKDTEEDFHVDOVTVKVPMMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
QY 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKSVAHVAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKSVAHVAVLTIDEKGTAAAGAMFLERIPMSI 360
QY 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTQK 394

RESULT 7
US-09-023-339-1
Sequence 1, Application US/09023339
Patent No. 6127145
GENERAL INFORMATION:
APPLICANT: Sutliff, Thomas D.
APPLICANT: Rodriguez, Raymond L.
TITLE OF INVENTION: Production of '1-Antitrypsin
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,339
FILING DATE: 13-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,991
FILING DATE: 13-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 0665-0003.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
CLONE: mature AAT amino acid sequence
US-09-023-339-1

Query Match 98.6%; Score 2003; DB 3; Length 394;
Best Local Similarity 98.5%; Pred. No. 3.6e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNFFSPVSIATA 60
DB 1 EDPOGDAQAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNFFSPVSIATA 60
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRLTNQPSQLQTTGNGFL 120
DB 61 FAMLSTGKADTHDEILEGNFNLTQIPEAQIHEGFQELLRLTNQPSQLQTTGNGFL 120
QY 121 SOGLKLVDFLEDKVKKLYHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 121 SOGLKLVDFLEDKVKKLYHSEAFVNFQDTEQAKQINDYVEKGTQKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKGKWRPFVKDTEEDFHVDOVTVKVPMMKRLGMFNIQHCKLSSWVL 240
DB 181 VFALVNYIFFKGKWRPFVKDTEEDFHVDOVTVKVPMMKRLGMFNIQHCKLSSWVL 240
QY 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
DB 241 LMKYLGNATAIFPLPDEGKQLHLENLTHDITKPLENEDRRSASLHLPKLSITGYDLK 300
QY 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKSVAHVAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKSVAHVAVLTIDEKGTAAAGAMFLERIPMSI 360
QY 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 361 PPEVKFNKPPFVFLMIEQNTKSPFLFMGKVVNPTQK 394

RESULT 8
US-08-121-714-3
Sequence 3, Application US/08121714
Patent No. 5470970
GENERAL INFORMATION:

Db 205 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGFMFNIOHCKKLSWVL 264
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 10

US-08-477-112-3
; Sequence 3, Application US/08477112
; Patent No. 5905023
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 425 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,112
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 06570/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 418
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-477-112-3

Query Match 98.6%; Score 2003; DB 2; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFSAFLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFSAFLYRQLAHQSNSTNIFSPVSIATA 84

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Db 85 FAWLSLGTAKDTHDEILGLENFNLTQIPEAQIHEGFQELLRTLNQPDLSOLQTTGNGLFL 144
QY 121 SOGLKLVDFKFLDVKKLYHSEAFVNFVFGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 145 SEGKLVDFKFLDVKKLYHSEAFVNFVFGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 204
QY 181 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGFMFNIOHCKKLSWVL 240
Db 205 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGFMFNIOHCKKLSWVL 264
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 11

US-10-030-330-3
; Sequence 3, Application US/10030330
; Patent No. 6833262
; GENERAL INFORMATION:
; APPLICANT: The University of Georgia Research Foundation, Inc
; TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
; FILE REFERENCE: 235.00210201
; CURRENT APPLICATION NUMBER: US/10/030,330
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/130,436
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-030-330-3

Query Match 98.6%; Score 2003; DB 4; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFSAFLYRQLAHQSNSTNIFSPVSIATA 60
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QY 61 FAWLSLGTAKDTHDEILGLENFNLTQIPEAQIHEGFQELLRTLNQPDLSOLQTTGNGLFL 120
Db 85 FAWLSLGTAKDTHDEILGLENFNLTQIPEAQIHEGFQELLRTLNQPDLSOLQTTGNGLFL 144

QY 121 SOGLKLVDFKFLDVKKLYHSEAFVNFVFGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 145 SEGKLVDFKFLDVKKLYHSEAFVNFVFGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 204

QY 181 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGFMFNIOHCKKLSWVL 240
Db 205 VPALVNYIPFKGKWERPFVKDTEBEDPHVDQVTTVKVPMKELGFMFNIOHCKKLSWVL 264

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
Db 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324

QY 301 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQLGITKVFSGNADLSGVTEAPLKLKSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 394
Db 385 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 418

RESULT 14
US-08-553-488A-1:
; Sequence 1, Application US/08553488A
; Patent No. 5817484
; GENERAL INFORMATION:
; APPLICANT: YU, Myeong-Hee
; APPLICANT: KWON, Ki-Sun
; APPLICANT: LEE, Kee-Nyung
; APPLICANT: SHIN, Hwa-Soo
; TITLE OF INVENTION: THERMORESISTANT ALPHA-1-ANTITRYPSIN
; TITLE OF INVENTION: MUTIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YU, Myeong-Hee
; STREET: 3-1003, Hankang Apartment, 49-8, Jamwon-dong,
; STREET: Seocho-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 137-030
; ADDRESSEE: KWON, Ki-Sun
; STREET: 130-1306, Hanbit Apartment, Oun-dong,
; STREET: Yuseong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 305-333
; ADDRESSEE: LEE, Kee-Nyung
; STREET: 105-1004, Hanbit Apartment, Oun-dong,
; STREET: Yuseong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 305-333
; ADDRESSEE: SHIN, Hwa-Soo
; STREET: 3-303, Sindonga Apartment, Yongjeon-dong,
; STREET: Dong-gu
; CITY: Taejeon
; STATE: Taejeon
; COUNTRY: Republic of Korea
; ZIP: 300-200
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,488A
; FILING DATE: 20-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 93-8510
; FILING DATE: 18-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: wild type human '-1-antitrypsin

US-08-553-488A-1
Query Match 98.0%; Score 1992; DB 2; Length 394;
Best Local Similarity 97.7%; Pred. No. 3.9e-180;
Matches 385; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAEPAFSLYRQLAHQSNSTIFFSPVSIATA 60
Db 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAEPAFSLYRQLAHQSNSTIFFSPVSIATA 60
QY 61 FAMLISLGTAKADTHDEILEGLNFNLTQIPPAQIHGEGFOELLRTLNQDPSQLQTTGNGLFL 120
Db 61 FAMLISLGTAKADTHDEILEGLNFNLTQIPPAQIHGEGFOELLRTLNQDPSQLQTTGNGLFL 120
QY 121 SOGLKLVDFLEDVVKLYHSEAFYVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 121 SEGLKLVDFLEDVVKLYHSEAFYVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
QY 181 VFALVNYIFFKQKWERPPFVKDTEEDFHVQDVTTVKVPMMKRLGFMNIOHCKKLSWVL 240
Db 181 VFALVNYIFFKQKWERPPFVKDTEEDFHVQDVTTVKVPMMKRLGFMNIOHCKKLSWVL 240
QY 241 LMKYLGNAITAFPLPDEGKLOHLELTHDITTKFLENERDRRSASLHLPKLSITGYDVK 300
Db 241 LMKYLGNAITAFPLPDEGKLOHLELTHDITTKFLENERDRRSASLHLPKLSITGYDVK 300
QY 301 SVLGQLGITKVFNSGADLSGVTEEAPLKLKAVHKAULTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQLGITKVFNSGADLSGVTEEAPLKLKAVHKAULTIDEKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 394
Db 361 PPEVKENKPPVFLMIBQNTKSPKPLFMGKVVNPTGK 394

RESULT 15
US-08-002-202-19
; Sequence 19, Application US/08002202
; Patent No. 5604201
; GENERAL INFORMATION:
; APPLICANT: Thomas, Garry
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti and Witcoff, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/002,202
; FILING DATE: 08-JAN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5604201nan, Kevin E
; REGISTRATION NUMBER: 35,30003
; REFERENCE/DOCKET NUMBER: 92,448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-002-202-19

Query Match      97.1%; Score 1973; DB 1; Length 414;
Best Local Similarity 97.5%; Pred. No. 2,7e-178;
Matches 384; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 1 EDPOGDAQKTDTHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
Db 25 EDPOGDAQKTDTHHDQDHPFNKITPNLAEFAFSLYRQLAHQSNSTNIPFSPVSIATA 84
QY 61 FAWLSLGTAKADTHDELLEGLENFLTQIPEAQIHEGFOELLRTLNQPDLSQLTGTGGLFL 120
Db 85 FAWLSLGTAKADTHDELLEGLENFLTQIPEAQIHEGFOELLRTLN----QLQTTGNGLFL 140
QY 121 SQGLKLVDFLEDVKKLYHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 141 SQGLKLVDFLEDVKKLYHSEAFVNFQDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 200
QY 181 VFALVNIYFFKQKWRPPEVKDTEBEDFHVQDVTTKVPMKRLGMFNIQHCKLSSWVL 240
Db 201 VFALVNIYFFKQKWRPPEVKDTEBEDFHVQDVTTKVPMKRLGMFNIQHCKLSSWVL 260
QY 241 LMKYLGNTAIFPLPDEGKLQHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 300
Db 261 LMKYLGNTAMFPLPDEGKLQHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTYDLK 320
QY 301 SVLGQLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 321 SVLGQLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 380
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLMGKVNVPTGK 394
Db 381 PPEVKFNKPFVFLMIEQNTKSPFLMGKVNVPTGK 414
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Search completed: June 20, 2005, 19:47:29
Job time : 46 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2003	98.6		394	14	US-10-025-514-2	Sequence 2, Appli
2	2003	98.6		395	17	US-10-914-863-2	Sequence 2, Appli
3	2003	98.6		418	14	US-10-097-340-286	Sequence 286, App
4	2003	98.6		418	15	US-10-411-037-22	Sequence 22, Appl
5	2003	98.6		418	15	US-10-411-026-22	Sequence 22, Appl
6	2003	98.6		418	15	US-10-410-962-22	Sequence 22, Appl
7	2003	98.6		418	15	US-10-411-049-22	Sequence 22, Appl
8	2003	98.6		418	16	US-10-410-930-22	Sequence 22, Appl
9	2003	98.6		418	16	US-10-410-997-22	Sequence 22, Appl
10	2003	98.6		418	16	US-10-411-012-22	Sequence 22, Appl
11	2003	98.6		418	16	US-10-287-994-22	Sequence 22, Appl

85 827 40.7 423 10 US-09-978-418-14 Sequence 14, App1
86 827 40.7 423 17 US-10-485-231-14 Sequence 14, App1
87 824 40.6 379 14 US-10-097-340-139 Sequence 139, App
88 824 40.6 406 17 US-10-741-600-1211 Sequence 1211, App
89 824 40.6 406 17 US-10-741-600-1212 Sequence 1212, App
90 824 40.6 406 17 US-10-741-600-1213 Sequence 1213, App
91 824 40.6 406 17 US-10-741-600-1214 Sequence 1214, App
92 824 40.6 406 17 US-10-741-600-1215 Sequence 1215, App
93 820 40.4 427 14 US-10-005-956-578 Sequence 578, App
94 819 40.3 411 15 US-10-210-172-122 Sequence 122, App
95 819 40.3 411 15 US-10-210-172-124 Sequence 124, App
96 819 40.3 411 15 US-10-210-172-126 Sequence 126, App
97 819 40.3 411 15 US-10-210-172-128 Sequence 128, App
98 819 40.3 411 15 US-10-210-172-130 Sequence 130, App
99 819 40.3 411 15 US-10-210-172-132 Sequence 132, App
100 819 40.3 411 15 US-10-210-172-134 Sequence 134, App

ALIGNMENTS

RESULT 1
US-10-025-514-2
; Sequence 2, Application US/10025514
; Publication No. US20030073217A1
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 36829200200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-514-2

Query Match 98.6%; Score 2003; DB 14; Length 394;
Best Local Similarity 98.5%; Pred. No. 2.5e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
Db 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIPFSPVSIATA 60

QY 61 FAMLISGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNOPDSQLQTTGNGLFL 120
Db 61 FAMLISGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNOPDSQLQTTGNGLFL 120

QY 121 SQGLKLVDFKLEEDVKLYHSEAFVNFQGTDEAKQIINDYVEKGTQGIIVDLVKELDRDT 180
Db 121 SQGLKLVDFKLEEDVKLYHSEAFVNFQGTDEAKQIINDYVEKGTQGIIVDLVKELDRDT 180

QY 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 240
Db 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 240

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENERDRRSASLHLPKLSITGTIDLK 300
Db 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENERDRRSASLHLPKLSITGTIDLK 300

QY 301 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLEIPRSI 360
Db 301 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLEIPMSI 360

QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394

RESULT 2
US-10-914-863-2
; Sequence 2, Application US/10914863
; Publication No. US20050084972A1
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: GIBSON, HELEN L.
; TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST
; FILE REFERENCE: 39042-0012
; CURRENT APPLICATION NUMBER: US/10/914,863
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/493,984
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence
; OTHER INFORMATION: encoded by rAA expression plasmid pYEP829
US-10-914-863-2

Query Match 98.6%; Score 2003; DB 17; Length 395;
Best Local Similarity 98.5%; Pred. No. 2.6e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIPFSPVSIATA 60
Db 2 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAEPFAFSLYRQLAHQSNSTNIPFSPVSIATA 61

QY 61 FAMLISGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNOPDSQLQTTGNGLFL 120
Db 62 FAMLISGKTADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNOPDSQLQTTGNGLFL 121

QY 121 SQGLKLVDFKLEEDVKLYHSEAFVNFQGTDEAKQIINDYVEKGTQGIIVDLVKELDRDT 180
Db 122 SQGLKLVDFKLEEDVKLYHSEAFVNFQGTDEAKQIINDYVEKGTQGIIVDLVKELDRDT 181

QY 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 240
Db 182 VFALVNYIIFPKGKWERPPEVKDTEEDFHVQDQVTTVKVPMKRLGMFNIQHCKLSSWVL 241

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENERDRRSASLHLPKLSITGTIDLK 300
Db 242 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENERDRRSASLHLPKLSITGTIDLK 301

QY 301 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLEIPRSI 360
Db 302 SVLGQLGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLEIPMSI 361

QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
Db 362 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 395

RESULT 3
US-10-097-340-286
; Sequence 286, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: John MONAHAN
; APPLICANT: Manjula GANNAVABAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS

APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. EAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, Assessment, Prevention, and Therapy of Ovarian Cancer

TITLE OF INVENTION: GALACTOSIDASE A

FILE REFERENCE: MRI-030

CURRENT APPLICATION NUMBER: US/10/097,340

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: 60/276,025

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/325,149

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/276,026

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 60/324,967

PRIOR FILING DATE: 2001/09/26

PRIOR APPLICATION NUMBER: 60/311,732

PRIOR FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/325,102

PRIOR FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 60/323,580

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 363

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 286

LENGTH: 418

TYPE: PRT

ORGANISM: Homo sapiens

US-10-097-340-286

Query Match 98.6%; Score 2003; DB 14; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDPTFNKITPNLAFAFSLYQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAAKTDTSHHDQDPTFNKITPNLAFAFSLYQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGTTKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQPDLSQQLTTGNGLFL 120
DB 85 FAMLISGTTKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQPDLSQQLTTGNGLFL 144
QY 121 SQGLKLVDFKLEEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFKLEEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKQKWRPFVKOTEEEDFHVDQVTTVKVPMKRLGMFNIOHCKLSSWVL 240
DB 205 VFALVNYIFFKQKWRPFVKOTEEEDFHVDQVTTVKVPMKRLGMFNIOHCKLSSWVL 264
QY 241 LMKYLGNTAIFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300
DB 265 LMKYLGNTAIFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 324
QY 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 418

RESULT 4

US-10-411-037-22

RESULT 5

US-10-411-037-22

; Sequence 22, Application US/10411037

; Publication No. US20040043446A1

; GENERAL INFORMATION:

; APPLICANT: Neose Technologies, Inc.

; APPLICANT: DeFrees, Shawn

; APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David

; APPLICANT: Chen, Xi

; APPLICANT: Bowe, Caryn

; TITLE OF INVENTION: ALPHA GALACTOSIDASE A

; FILE REFERENCE: 040853-01-5082

; CURRENT APPLICATION NUMBER: US/10/411,037

; CURRENT FILING DATE: 2003-04-09

; PRIOR APPLICATION NUMBER: US 60/328,523

; PRIOR FILING DATE: 2001-10-10

; PRIOR APPLICATION NUMBER: US 60/344,692

; PRIOR FILING DATE: 2001-10-19

; PRIOR APPLICATION NUMBER: US 60/387,292

; PRIOR FILING DATE: 2002-06-07

; PRIOR APPLICATION NUMBER: US 60/391,777

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: US 60/396,594

; PRIOR FILING DATE: 2002-07-17

; PRIOR APPLICATION NUMBER: US 60/404,249

; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527

; PRIOR FILING DATE: 2002-08-28

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 22

; LENGTH: 418

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-411-037-22

Query Match 98.6%; Score 2003; DB 15; Length 418;

Best Local Similarity 98.5%; Pred. No. 2.8e-154;

Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDPTFNKITPNLAFAFSLYQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAAKTDTSHHDQDPTFNKITPNLAFAFSLYQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAMLISGTTKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQPDLSQQLTTGNGLFL 120
DB 85 FAMLISGTTKADTHDELEGNFNLTOIPEAQIHEGFQELLRTLNQPDLSQQLTTGNGLFL 144
QY 121 SQGLKLVDFKLEEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGLKLVDFKLEEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKQKWRPFVKOTEEEDFHVDQVTTVKVPMKRLGMFNIOHCKLSSWVL 240
DB 205 VFALVNYIFFKQKWRPFVKOTEEEDFHVDQVTTVKVPMKRLGMFNIOHCKLSSWVL 264
QY 241 LMKYLGNTAIFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 300
DB 265 LMKYLGNTAIFPLPDEGKLOHLENELTHDITTKFLENEDRRSASLHLPKLSITGTIDLK 324
QY 301 SVLGQIGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFMGKVVNPTGK 418

RESULT 5

US-10-411-037-22

; Sequence 22, Application US/10411037

Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US 10/411,026
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-22

Query Match 98.6%; Score 2003; DB 15; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTSDSHDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAAKTSDSHDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGNLNLTOIPRAQIHGEGFQELLRLTNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGNLNLTEIPEAQIHGEGFQELLRLTNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGKIYDLVKELDRDT 180
DB 145 SEGLKLVDFLEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGKIYDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 240
DB 205 VFALVNYIFFKGKWRPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 264
QY 241 LMKYLGNAITAFPLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 6
US-10-410-962-22
; Sequence 22, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.

APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US 10/410,962
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-22

Query Match 98.6%; Score 2003; DB 15; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAAKTSDSHDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAAKTSDSHDDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGNLNLTOIPRAQIHGEGFQELLRLTNQDPSQLQTTGNGLFL 120
DB 85 FAMLSTGKADTHDEILEGNLNLTEIPEAQIHGEGFQELLRLTNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGKIYDLVKELDRDT 180
DB 145 SEGLKLVDFLEDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGKIYDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWRPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 240
DB 205 VFALVNYIFFKGKWRPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIOHCKLSSWYL 264
QY 241 LMKYLGNAITAFPLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLQHLENELTHDITTKFLENEDRRSASLHLPKLSITGYDLK 324
QY 301 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 7
US-10-411-049-22
; Sequence 22, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.

APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Carlyn
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-10-411-049-22

Query Match 98.6%; Score 2003; DB 15; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKIPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKIPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAWLSGKTADTHDELEGNFNLTOIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAWLSGKTADTHDELEGNFNLTOIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFKEDVKKLYHSEAFVNFVFGDTEQAKQINDYVEKGQKIVDLVKELDRDT 180
DB 145 SEGKLVDFKEDVKKLYHSEAFVNFVFGDTEQAKQINDYVEKGQKIVDLVKELDRDT 204
QY 181 VPALVNYIPFKGKWRPFVVDKTEBEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWYL 240
DB 205 VPALVNYIPFKGKWRPFVVDKTEBEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWYL 264
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRSASLHLPKLSITGYDLK 324
QY 301 SVLGOLGITKVFNSGADLSGVTEEAPLKLKSAVHKAVALTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFNSGADLSGVTEEAPLKLKSAVHKAVALTIDEKTEAAGAMFLERIPRSI 384
QY 361 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 8

US-10-410-930-22
Sequence 22, Application US/10410930
Publication No. US20040115168A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn

APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Carlyn
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5056
CURRENT APPLICATION NUMBER: US/10/410,930
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 418
TYPE: PRT
ORGANISM: Homo sapiens
US-10-410-930-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKIPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKIPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAWLSGKTADTHDELEGNFNLTOIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 120
DB 85 FAWLSGKTADTHDELEGNFNLTOIPEAQIHEGFOELLRTLNQPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFKEDVKKLYHSEAFVNFVFGDTEQAKQINDYVEKGQKIVDLVKELDRDT 180
DB 145 SEGKLVDFKEDVKKLYHSEAFVNFVFGDTEQAKQINDYVEKGQKIVDLVKELDRDT 204
QY 181 VPALVNYIPFKGKWRPFVVDKTEBEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWYL 240
DB 205 VPALVNYIPFKGKWRPFVVDKTEBEDFHVQDQVTVKVPMMKRLGMFNIQHCKLSSWYL 264
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDITTKFLENEDRSASLHLPKLSITGYDLK 324
QY 301 SVLGOLGITKVFNSGADLSGVTEEAPLKLKSAVHKAVALTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFNSGADLSGVTEEAPLKLKSAVHKAVALTIDEKTEAAGAMFLERIPRSI 384
QY 361 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKFPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 9

US-10-410-997-22
Sequence 22, Application US/10410997
Publication No. US20040126838A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David

; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-997-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGKTADTHDEILEGNLNLTOIPEAQIHEGFOELLRTLNOPDSQLOLTTGNGLFL 120
DB 85 FAMLISGKTADTHDEILEGNLNLTEIPEAQIHEGFOELLRTLNOPDSQLOLTTGNGLFL 144
QY 121 SGLKLVDKFLDVKLVKLYHSEAFVNFVGTDEAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SGLKLVDKFLDVKLVKLYHSEAFVNFVGTDEAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VPALVNYIFFKGKWRPPEVKDTEBEDFHVQDQVTVTKVPMKRLGMFNIQHCKLSSWYL 240
DB 205 VPALVNYIFFKGKWRPPEVKDTEBEDFHVQDQVTVTKVPMKRLGMFNIQHCKLSSWYL 264
QY 241 LMKYLGNATAIFLDPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDJK 300
DB 265 LMKYLGNATAIFLDPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDJK 324
QY 301 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKTEAAGAMFLERIPRSI 384
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 10
US-10-411-012-22
; Sequence 22, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-012-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGKTADTHDEILEGNLNLTOIPEAQIHEGFOELLRTLNOPDSQLOLTTGNGLFL 120
DB 85 FAMLISGKTADTHDEILEGNLNLTEIPEAQIHEGFOELLRTLNOPDSQLOLTTGNGLFL 144
QY 121 SGLKLVDKFLDVKLVKLYHSEAFVNFVGTDEAKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SGLKLVDKFLDVKLVKLYHSEAFVNFVGTDEAKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VPALVNYIFFKGKWRPPEVKDTEBEDFHVQDQVTVTKVPMKRLGMFNIQHCKLSSWYL 240
DB 205 VPALVNYIFFKGKWRPPEVKDTEBEDFHVQDQVTVTKVPMKRLGMFNIQHCKLSSWYL 264
QY 241 LMKYLGNATAIFLDPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDJK 300
DB 265 LMKYLGNATAIFLDPDEGKLOHLENELTHDITKPLENEDRRSASLHLPKLSITGYDJK 324
QY 301 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKTEAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKTEAAGAMFLERIPRSI 384
QY 361 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 418

RESULT 11
US-10-287-994-22
; Sequence 22, Application US/10287994
; Publication No. US20040137557A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert

; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5052-00
; CURRENT APPLICATION NUMBER: US/10/287,994
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-994-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPQAQHEGFQELLRTLNQDPSQLTGTGNGFL 120
DB 85 FAMLSTGKADTHDEILEGNFNLTQIPQAQHEGFQELLRTLNQDPSQLTGTGNGFL 144
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTGKIVDLVKELDRT 180
DB 145 SEGKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTGKIVDLVKELDRT 204
QY 181 VFALVNYIFFKGKWERPPEVKDTEBEDFHDVQVTVTKVPMKRLGMFNIQHCKKLSWYL 240
DB 205 VFALVNYIFFKGKWERPPEVKDTEBEDFHDVQVTVTKVPMKRLGMFNIQHCKKLSWYL 264
QY 241 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTYDLK 300
DB 265 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTYDLK 324
QY 301 SVLGQGITKVFSGNADLSGVTEEAFLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFSGNADLSGVTEEAFLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNKTSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIQNKTSPFLFMGKVVNPTGK 418

RESULT 12
US-10-410-913-22
; Sequence 22, Application US/10410913
; Publication No. US20040142856A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn

; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5081
; CURRENT APPLICATION NUMBER: US/10/410,913
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-913-22

Query Match 98.6%; Score 2003; DB 16; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHTFNKITPNLAFAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLSTGKADTHDEILEGNFNLTQIPQAQHEGFQELLRTLNQDPSQLTGTGNGFL 120
DB 85 FAMLSTGKADTHDEILEGNFNLTQIPQAQHEGFQELLRTLNQDPSQLTGTGNGFL 144
QY 121 SQGLKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTGKIVDLVKELDRT 180
DB 145 SEGKLVDFLEVDKVLHSEAFVNFQDTEQAQKQINDYVEKGTGKIVDLVKELDRT 204
QY 181 VFALVNYIFFKGKWERPPEVKDTEBEDFHDVQVTVTKVPMKRLGMFNIQHCKKLSWYL 240
DB 205 VFALVNYIFFKGKWERPPEVKDTEBEDFHDVQVTVTKVPMKRLGMFNIQHCKKLSWYL 264
QY 241 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTYDLK 300
DB 265 LMKYLGNAITAIFLPDEGKLOHLENLTHDITTKFLENERDRSASLHLPKLSITGTYDLK 324
QY 301 SVLGQGITKVFSGNADLSGVTEEAFLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQGITKVFSGNADLSGVTEEAFLKSKAVHKAVALTIDKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNKTSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIQNKTSPFLFMGKVVNPTGK 418

RESULT 13
US-10-410-980-22
; Sequence 22, Application US/10410980
; Publication No. US20050031584A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2

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; FILE REFERENCE: 040853-01-5066
; CURRENT APPLICATION NUMBER: US/10/410,980
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-980-22

Query Match      98.6%; Score 2003; DB 17; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 85 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 145 SEGKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIOHCKKLSWWVL 240
Db 205 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIOHCKKLSWWVL 264
QY 241 LMKYLGNAITAIFFLPDEGKLQHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTIDLK 300
Db 265 LMKYLGNAITAIFFLPDEGKLQHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTIDLK 324
QY 301 SVLGQGITKTVFSGNADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQGITKTVFSGNADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNTKSPLEFMGKVVNPTGK 394
Db 385 PPEVKFNKPFVFLMIQNTKSPLEFMGKVVNPTGK 418

RESULT 14
US-10-971-461-15
; Sequence 15, Application US/10971461
; Publication No. US20050070477A1
; GENERAL INFORMATION:
; APPLICANT: Cochrane, Charles G.
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
; FILE REFERENCE: 1361.037US1
; CURRENT APPLICATION NUMBER: US/10/971,461
; PRIOR FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-971-461-15

Query Match      98.6%; Score 2003; DB 17; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 60
Db 25 EDPOGDAQAQKTDTSHHDDQHPFTFNKITPNLAFSAFSLYRQLAHQSNSTNIFSPVSIATA 84
QY 61 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 85 FAMLISGTTKADTHDEILEGNFNLTQIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 145 SEGKLVDFLEVDVKLYHSEAFVNFNGDTEEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIOHCKKLSWWVL 240
Db 205 VFALVNYIFFKGKWERPFVKDTEEDFHVDQVTTVKVPMKRLGMFNIOHCKKLSWWVL 264
QY 241 LMKYLGNAITAIFFLPDEGKLQHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTIDLK 300
Db 265 LMKYLGNAITAIFFLPDEGKLQHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTIDLK 324
QY 301 SVLGQGITKTVFSGNADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQGITKTVFSGNADLSGVTEEAAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIQNTKSPLEFMGKVVNPTGK 394
Db 385 PPEVKFNKPFVFLMIQNTKSPLEFMGKVVNPTGK 418

RESULT 15
US-10-410-897-22
; Sequence 22, Application US/10410897
; Publication No. US20050100982A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FACTOR IX; REMODELING AND GLYCOCONJUGATION OF FACTOR IX
; FILE REFERENCE: 040853-01-5058
; CURRENT APPLICATION NUMBER: US/10/410,897
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-410-897-22

Query Match		98.6%	Score 2003;	DB 17;	Length 418;
Best Local Similarity		98.5%	Pred. No. 2.8e-154;		
Matches 388;		Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0;
Qy	1	EDPQGDAACKTDSHDDQDHPTEFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA	60		
Db	25	EDPQGDAACKTDSHDDQDHPTEFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA	84		
Qy	61	FAMLSLGTAKADTHDELLEGINFNLTOIPEAQIHEGFQELLRTLNQPDSQLQTTGNGLFL	120		
Db	85	FAMLSLGTAKADTHDELLEGINFNLTEIPEAQIHEGFQELLRTLNQPDSQLQTTGNGLFL	144		
Qy	121	SOGLKLVDPLEVDVKLYHSEAPTVNFGDTEQAQKQINDYVEKGTQCKIVDLVKELDRT	180		
Db	145	SEGLKLVDFLEVDVKLYHSEAPTVNFGDTEEAQKQINDYVEKGTQCKIVDLVKELDRT	204		
Qy	181	VFALVNYIIFPKGKWERPFVVKDTEEREDFHVQDVTTVKVPMMKELGMFNIQHCCKLSSWVL	240		
Db	205	VFALVNYIIFPKGKWERPFVVKDTEEREDFHVQDVTTVKVPMMKELGMFNIQHCCKLSSWVL	264		
Qy	241	LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK	300		
Db	265	LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK	324		
Qy	301	SVLGQLGITKVFSGNADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI	360		
Db	325	SVLGQLGITKVFSGNADLSGVTEEAFLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPMSI	384		
Qy	361	PPEVKENKPPVFLMIEQNTKSPFLFMGKVNPQK	394		
Db	385	PPEVKENKPPVFLMIEQNTKSPFLFMGKVNPQK	418		

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Job time : 163 secs

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OM protein - protein search, using sw model

Run on: June 20, 2005, 19:41:46 ; Search time 488 Seconds
(without alignments)
943.021 Million cell updates/sec

Title: PDX1
Perfect score: 2032
Sequence: 1 EDPOQDAQAQTTSHHDDH.....IBQNTKSLFMGKVVNPTGK 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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- 1: /cgn2_6/ptodata/1/paa/PTCUS COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2026	99.7	394	17	US-09-372-003-11	Sequence 11, Appli
4	2021	99.5	394	16	US-09-290-034C-1	Sequence 1, Appli
5	2020	99.4	394	17	US-09-372-003-6	Sequence 6, Appli
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ALIGNMENTS

RESULT 1
US-09-372-003-9
; Sequence 9, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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; NAME/KEY: Modified site
; LOCATION: 355..358
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; Sequence 6, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-034C-6

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RESULT 3
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; Sequence 11, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
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; LOCATION: 355..358 /label=Variant
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; US-09-372-003-11

Query Match 99.7%; Score 2026; DB 17; Length 394;
Best Local Similarity 99.7%; Pred. No. 1.4e-176;
Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 1, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 92448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 394
; TYPE: PPT
; ORGANISM: Homo sapiens
; US-09-290-034C-1

Query Match 99.5%; Score 2021; DB 16; Length 394;
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Db 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIIDKGTAAAGAMFLERIPRSI 360
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RESULT 5
US-09-372-003-6
; Sequence 6, Application US/09372003
; GENERAL INFORMATION:
; APPLICANT: Thomas, Gary
; APPLICANT: Anderson, Eric D
; APPLICANT: Thomas, Laurel
; APPLICANT: Haylick, Joel S
; APPLICANT: Nelson, Jay
; APPLICANT: Stenglen, Stephan G
; TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
; TITLE OF INVENTION: Endoprotease
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,003
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/481,534
; FILING DATE: 14-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Noonan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,448-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 394 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-372-003-6
Query Match 99.4%; Score 2020; DB 17; Length 394;
Best Local Similarity 99.5%; Pred. No. 5.1e-176;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
QY 61 FAMLISLGTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 61 FAMLISLGTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDRT 180
Db 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDRT 180
QY 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKLSSWYL 240
Db 181 VFALVNYIIFPKGKWERPPEVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKLSSWYL 240
QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
Db 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGTYDLK 300
QY 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIIDKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFSGADLSGVTEEAFLKSKAVHKAVLTIIDKGTAAAGAMFLERIPRSI 360
QY 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVPNTGK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVPNTGK 394

RESULT 6
US-10-025-514-2
; Sequence 2, Application US/10025514
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Helen GIBSON
; APPLICANT: Philip PEMBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 368292000200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: U.S. 60/331,966
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-514-2

Query Match 98.6%; Score 2003; DB 26; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.9e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPQGDAAQKTDTSHHDDQHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
QY 61 FAMLISLGTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 61 FAMLISLGTADTHDEILEGNLNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQCKIVDLVKELDRT 180

Db 121 :|||: SEGLKLVDFLEVDKKLYHSEAFVNFQDTEAEKKQINDYVEKGTQGI VDLVKELDRDT 180
Qy 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Qy 241 LMKYLGNATAIFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 241 LMKYLGNATAIFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Qy 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPMSI 360
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394
Db 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394
RESULT 7
US-10-914-863-2
; Sequence 2, Application US/10914863
; GENERAL INFORMATION:
; APPLICANT: GIBSON, HELEN L.
; TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST
; FILE REFERENCE: 39042-0012
; CURRENT APPLICATION NUMBER: US/10/914,863
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/493,984
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence
; OTHER INFORMATION: encoded by rAA expression plasmid pYEP829
US-10-914-863-2
Query Match 98.6%; Score 2003; DB 35; Length 395;
Best Local Similarity 98.5%; Pred. No. 1.9e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EDQGDAAQKTDTSHHDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 60
Db 2 EDQGDAAQKTDTSHHDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 61
Qy 61 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLTTGNGLFL 120
Db 62 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLTTGNGLFL 121
Qy 121 SQGLKLVDFLEVDKKLYHSEAFVNFQDTEAEKKQINDYVEKGTQGI VDLVKELDRDT 180
Db 122 SEGLKLVDFLEVDKKLYHSEAFVNFQDTEAEKKQINDYVEKGTQGI VDLVKELDRDT 181
Qy 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 182 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 241
Qy 241 LMKYLGNATAIFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 242 LMKYLGNATAIFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 301
Qy 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 302 SVLGQIGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPMSI 361
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394

Db 362 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 395
RESULT 8
PCT-US02-07826-286
; Sequence 286, Application PC/TUS0207826
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc. et al.
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030PC
; CURRENT APPLICATION NUMBER: PCT/US02/07826
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-07826-286
Query Match 98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EDQGDAAQKTDTSHHDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 60
Db 25 EDQGDAAQKTDTSHHDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNFFSPVSIATA 84
Qy 61 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLTTGNGLFL 120
Db 85 FAMLSTGTAKDTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLTTGNGLFL 144
Qy 121 SQGLKLVDFLEVDKKLYHSEAFVNFQDTEAEKKQINDYVEKGTQGI VDLVKELDRDT 180
Db 145 SEGLKLVDFLEVDKKLYHSEAFVNFQDTEAEKKQINDYVEKGTQGI VDLVKELDRDT 204
Qy 181 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 205 VFALVNYIFFKQKWERPFVKDTEEDFHVQDVQVTVTKVPMKRLGMFNIQHCKKLSWVL 264
Qy 241 LMKYLGNATAIFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 265 LMKYLGNATAIFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 324
Qy 301 SVLGQIGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 325 SVLGQIGITKVFNSGADLSGVTEAPLKLKAVHKAVLTIDEKGTAAAGAMFLERIPMSI 384
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 394
Db 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPQK 418
RESULT 9
PCT-US02-32263-22
; Sequence 22, Application PC/TUS0232263
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.

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; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Bower, Caryn
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5050W0
; CURRENT APPLICATION NUMBER: PCT/US02/32263
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 22
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-32263-22
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Query Match      98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAWLSLGTAKADTHDEILEGNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAWLSLGTAKADTHDEILEGNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDKFLVDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SEGKLVDKFLVDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VFALVNYIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWVL 240
DB 205 VFALVNYIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWVL 264
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGNADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNNPTGK 418

RESULT 10
PCT-US03-12324-20
; Sequence 20, Application PC/TUS0312324
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Cochran, Charles G.
; APPLICANT: Oades, Zenaïda G.
; APPLICANT: Revak, Susan D.
; APPLICANT: Niven, Ralph
; TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
; FILE REFERENCE: 1361.037W01
; CURRENT APPLICATION NUMBER: PCT/US03/12731
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,968
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 418
; TYPE: PRT
```

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; APPLICANT: UNIVERSITY OF FLORIDA
; APPLICANT: ATKINSON, MARK A.
; APPLICANT: FLOTTE, TERENCE R.
; APPLICANT: SONG, SIHONG
; APPLICANT: LOILER, SCOTT A.
; TITLE OF INVENTION: FAAV VECTOR-BASED COMPOSITIONS AND METHODS FOR THE PREVENTION AND
; TREATMENT OF MAMMALIAN DISEASES
; FILE REFERENCE: 4300.014510
; CURRENT APPLICATION NUMBER: PCT/US03/12324
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,083
; PRIOR FILING DATE: 2003-04-19
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US03-12324-20

Query Match      98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 84
QY 61 FAWLSLGTAKADTHDEILEGNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAWLSLGTAKADTHDEILEGNFNLTQIPRAQIHGFGQELLRTLNQDPSQLQTTGNGLFL 144
QY 121 SOGLKLVDKFLVDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 180
DB 145 SEGKLVDKFLVDVKKLYHSEAFVNFNGDTEQAQKQINDYVEKGTQKIVDLVKELDRDT 204
QY 181 VFALVNYIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWVL 240
DB 205 VFALVNYIFPKGKWERPFVKDTEEDFHVQDVTTVKVPMMKRLGMFNIQHCKKLSWWVL 264
QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 324
QY 301 SVLGQIGITKVFSGNADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFSGNADLSGVTEEAAPLKLSKAVHKAVLTIDEKGTAAAGAMFLERIPRSI 384
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNNPTGK 418

RESULT 11
PCT-US03-12731-15
; Sequence 15, Application PC/TUS0312731
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; APPLICANT: Cochran, Charles G.
; APPLICANT: Oades, Zenaïda G.
; APPLICANT: Revak, Susan D.
; APPLICANT: Niven, Ralph
; TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
; FILE REFERENCE: 1361.037W01
; CURRENT APPLICATION NUMBER: PCT/US03/12731
; CURRENT FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: US 60/375,968
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 418
; TYPE: PRT
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PCT-US04-11494-22

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Query Match          98.6%; Score 2003; DB 1; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLABFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAAKTDTSHHDQDHPFNKITPNLABFAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAWLSGKTADTHDEILEGNFNLTQIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAWLSGKTADTHDEILEGNFNLTQIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 144

QY 121 SOGLKLVDFLEDVKKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGKIVDLVKELDRDT 180
DB 145 SEGLKLVDFLEDVKKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGKIVDLVKELDRDT 204

QY 181 VFALVNYIIPFKGKWERPPEVKOTEEEDFHVDOVTVTKVPMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIIPFKGKWERPPEVKOTEEEDFHVDOVTVTKVPMKRLGMFNIQHCKKLSWWL 264

QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324

QY 301 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNNPTQK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNNPTQK 418
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RESULT 14
US-08-459-292-2
; Sequence 2, Application US/08459292
; GENERAL INFORMATION:
; APPLICANT: Brigham, Kenneth
; APPLICANT: Conary, Jon
; APPLICANT: Canonico, Angelo
; APPLICANT: Meyrick, Barbara
; TITLE OF INVENTION: DNA Construct for In Vivo Expression of
; TITLE OF INVENTION: a Human Gene
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
; STREET: 100 South Wacker Drive - Suite 960
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60606-4002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,292
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 690,283
; FILING DATE: 24-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: VU9111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 456-8000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-292-2

Query Match          98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLABFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAAKTDTSHHDQDHPFNKITPNLABFAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAWLSGKTADTHDEILEGNFNLTQIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 120
DB 85 FAWLSGKTADTHDEILEGNFNLTQIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 144

QY 121 SOGLKLVDFLEDVKKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGKIVDLVKELDRDT 180
DB 145 SEGLKLVDFLEDVKKLYHSEAFVNFVGTQTEAKKQINDYVEKGTQGKIVDLVKELDRDT 204

QY 181 VFALVNYIIPFKGKWERPPEVKOTEEEDFHVDOVTVTKVPMKRLGMFNIQHCKKLSWWL 240
DB 205 VFALVNYIIPFKGKWERPPEVKOTEEEDFHVDOVTVTKVPMKRLGMFNIQHCKKLSWWL 264

QY 241 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 300
DB 265 LMKYLGNAITAIFFLPDEGKLOHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLK 324

QY 301 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGQIGITKVFNSGADLSGVTEEAPLKLSKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNNPTQK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVNNPTQK 418

RESULT 15
US-08-472-758-3
; Sequence 3, Application US/08472758
; GENERAL INFORMATION:
; APPLICANT: Sager, Ruth
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN
; TITLE OF INVENTION: WITH
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,758
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/121,714
; FILING DATE: 09/01/93
; APPLICATION NUMBER: 07/938,823
; FILING DATE: 09/01/92
; APPLICATION NUMBER: 07/844,296
; FILING DATE: 02/28/92
; APPLICATION NUMBER: 07/662,216
; FILING DATE: 02/28/91
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TUMOR SUPPRESSING

ATTORNEY/AGENT INFORMATION:

NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06570/002003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 418
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-472-758-3

Query Match 98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.le-174;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 EDQGGAAQKTDTSHDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
25 EDQGGAAQKTDTSHDQDHTFNKITPNLAEPFSLYRQLAHQSNSTNIFSPVSIATA 84
Qy 61 FAMLSTGKTADYTHDEILEGLNFNLTOIPEAQIHGEGFQELLRTLNQPSQLQLTGNGLFL 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
85 FAMLSTGKTADYTHDEILEGLNFNLTOIPEAQIHGEGFQELLRTLNQPSQLQLTGNGLFL 144
Qy 121 SQGLKLVDFLEVDVKLYHSEAFVNFQDTEOAKQINDYVEKGTQGIYDLVKELDRDT 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
145 SEGKLVDFLEVDVKLYHSEAFVNFQDTEOAKQINDYVEKGTQGIYDLVKELDRDT 204
Qy 181 VPALVNYIPFGKWRPPEVKDTEEDFHVQVTVKVPMMKELGMFNIQHCKKLSWVL 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
205 VPALVNYIPFGKWRPPEVKDTEEDFHVQVTVKVPMMKELGMFNIQHCKKLSWVL 264
Qy 241 LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDLK 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
265 LMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDLK 324
Qy 301 SVLGQLGITKVFSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
325 SVLGQLGITKVFSGADLSGVTEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPMSI 384
Qy 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPTGK 394
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPTGK 418

Search completed: June 20, 2005, 19:55:44
Job time : 492 secs

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2003	98.6	394	1	PCT-US05-07959-2	Sequence 2, Appli	
2	2003	98.6	394	7	US-11-077-276-2	Sequence 2, Appli	
3	2003	98.6	418	7	US-11-050-926-286	Sequence 286, App	
4	2003	98.6	418	8	US-60-680-004-3	Sequence 3, Appli	
5	2003	98.6	418	8	US-60-685-372-1012	Sequence 1012, Ap	
6	2003	98.6	418	8	US-60-685-372-1014	Sequence 1014, Ap	
7	2003	98.6	418	8	US-60-685-372-1016	Sequence 1016, Ap	
8	2003	98.6	503	1	PCT-US05-07959-8	Sequence 8, Appli	
9	2003	98.6	503	1	PCT-US05-07959-16	Sequence 16, Appli	
10	2003	98.6	503	7	US-11-077-276-8	Sequence 8, Appli	
11	2003	98.6	503	7	US-11-077-276-16	Sequence 16, Appli	
12	2003	98.6	522	1	PCT-US05-07959-14	Sequence 14, Appli	
13	2003	98.6	522	1	PCT-US05-07959-20	Sequence 20, Appli	
14	2003	98.6	522	7	US-11-077-276-14	Sequence 14, Appli	
15	2003	98.6	522	7	US-11-077-276-20	Sequence 20, Appli	
16	2003	98.6	580	1	PCT-US05-07959-10	Sequence 10, Appli	
17	2003	98.6	580	1	PCT-US05-07959-18	Sequence 18, Appli	
18	2003	98.6	580	7	US-11-077-276-10	Sequence 10, Appli	
19	2003	98.6	580	7	US-11-077-276-18	Sequence 18, Appli	
20	2000	98.4	418	1	PCT-US03-10870-2304	Sequence 2304, Ap	
21	1999	98.4	419	8	US-60-680-004-1	Sequence 1, Appli	
22	1999	98.4	419	8	US-60-680-004-2	Sequence 2, Appli	
23	1999	98.4	419	8	US-60-680-004-4	Sequence 4, Appli	
24	1999	98.4	419	8	US-60-680-004-5	Sequence 5, Appli	
25	1999	98.4	419	8	US-60-680-004-6	Sequence 6, Appli	

99 481 23.7 415 8 US-60-664-579-565 Sequence 565, App
100 480.5 23.6 382 8 US-60-664-579-566 Sequence 566, App

ALIGNMENTS

RESULT 1
PCT-US05-07959-2
; Sequence 2, Application PCT/US0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-2

Query Match 98.6%; Score 2003; DB 1; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.3e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60

QY 61 FAMLISGKTADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 120
Db 61 FAMLISGKTADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 120

QY 121 SQGLKLVDFLEDKVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 121 SQGLKLVDFLEDKVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180

QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240
Db 181 VFALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240

QY 241 LMKYLGNAATAIFPLPDEGKLQHLNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 300
Db 241 LMKYLGNAATAIFPLPDEGKLQHLNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 300

QY 301 SVLGQGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360

QY 361 PPEVKFNKPPVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 361 PPEVKFNKPPVFLMIEQNTKSPFLFMGKVVNPTQK 394

RESULT 2
US-11-077-276-2
; Sequence 2, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077, 276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09

; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 2
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-2

Query Match 98.6%; Score 2003; DB 7; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.3e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 1 EDPOGDAQAOKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60

QY 61 FAMLISGKTADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 120
Db 61 FAMLISGKTADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 120

QY 121 SQGLKLVDFLEDKVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 121 SQGLKLVDFLEDKVKKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180

QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240
Db 181 VFALVNYIFFKGKWERPFVKDTEEDFHDVDQVTTVKVPMKRLGFMNIOHCKKLSWYL 240

QY 241 LMKYLGNAATAIFPLPDEGKLQHLNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 300
Db 241 LMKYLGNAATAIFPLPDEGKLQHLNLTQIPEAQIHEGFQELLRTLNQDLSQQLTGTGNGLFL 300

QY 301 SVLGQGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360
Db 301 SVLGQGITKVFSGNADLSGVTEEAPLKLKSAVHKAVLTIDEKGTAAAGAMFLERIPRSI 360

QY 361 PPEVKFNKPPVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 361 PPEVKFNKPPVFLMIEQNTKSPFLFMGKVVNPTQK 394

RESULT 3
US-11-050-926-286
; Sequence 286, Application US/11050926
; GENERAL INFORMATION:
; APPLICANT: Manjula GANNAVAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; FILE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/11/050,926
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14

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; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 286
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-926-286

Query Match      98.6%; Score 2003; DB 7; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 144

QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204
DB 145 SEGKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 264

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDILK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDILK 324

QY 301 SVLGOLGITKVFSGADLSGVTEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGADLSGVTEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 5
US-60-685-372-1012
; Sequence 1012, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall D
; APPLICANT: Cousineau, Johanne
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1012
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-685-372-1012

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 144

QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 264

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84
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QY 61 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 144

QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 264

QY 241 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDILK 300
DB 265 LMKYLGNAITAFPLPDEGKLOHLENELTHDIIITKPLENEDRRSASLHLPKLSITGYDILK 324

QY 301 SVLGOLGITKVFSGADLSGVTEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 325 SVLGOLGITKVFSGADLSGVTEAPLKLKAVHKAVLTIDKGTAAAGAMFLERIPRSI 384

QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 394
DB 385 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTGK 418

RESULT 5
US-60-685-372-1012
; Sequence 1012, Application US/60685372
; GENERAL INFORMATION:
; APPLICANT: Belouchi, Abdelmajid
; APPLICANT: Raelson, John V
; APPLICANT: Bradley, Walter E
; APPLICANT: Paquin, Bruno
; APPLICANT: Nguyen-Huu, Quynh
; APPLICANT: Croteau, Pascal
; APPLICANT: Allard, Rene
; APPLICANT: Little, Randall D
; APPLICANT: Cousineau, Johanne
; APPLICANT: Berdewegh, Paul V
; APPLICANT: Segal, Jonathan
; TITLE OF INVENTION: Genemap of the Human Genes Associated with Psoriasis
; FILE REFERENCE: 059908-5005-PR
; CURRENT APPLICATION NUMBER: US/60/685,372
; CURRENT FILING DATE: 2005-05-31
; NUMBER OF SEQ ID NOS: 2738
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1012
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-685-372-1012

Query Match      98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 60
DB 25 EDPOGDAQAQKTDTSHHDDQDHPFNKLTNPNAEFAFSLYRQLAHQSNSTNIFSPVSIATA 84

QY 61 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 120
DB 85 FAMLISLGTADTHDEILEGNFNLTQIPRAQIHEGFQELLRTLNQDPSQLQTTGNGLEFL 144

QY 121 SOGLKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 145 SEGKLVDFLEVDVKLYHSEAFVNFVGTQEAQKQINDYVEKGTQGIKIVDLVKELDRDT 204

QY 181 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
DB 205 VFALVNYIFFKGKWRPPEVKDTEBEDFHVQVTVTKVPMKRLGMFNIQHCKKLSWVL 264
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; SEQ ID NO 8
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-8

Query Match      98.6%; Score 2003; DB 1; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 110  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 169
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 120
Db 170  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 229
QY 121  SOGLKLVDFLEVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 230  SEGKLVDKFLVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 289
QY 181  VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 290  VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCKKLSWVL 349
QY 241  LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 300
Db 350  LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 409
QY 301  SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIIDEKGTAAAGAMFLERIPRSI 360
Db 410  SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIIDEKGTAAAGAMFLERIPRSI 469
QY 361  PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 470  PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 503

RESULT 9
PCT-US05-07959-16
; Sequence 16, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 16
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-16

Query Match      98.6%; Score 2003; DB 1; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 2  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 61
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 120
Db 62  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 121
QY 121  SOGLKLVDFLEVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 122  SEGKLVDKFLVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 181

; SEQ ID NO 8
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-8

Query Match      98.6%; Score 2003; DB 1; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 110  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 169
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 120
Db 170  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 229
QY 121  SOGLKLVDFLEVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 230  SEGKLVDKFLVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 289
QY 181  VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 290  VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCKKLSWVL 349
QY 241  LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 300
Db 350  LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 409
QY 301  SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIIDEKGTAAAGAMFLERIPRSI 360
Db 410  SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIIDEKGTAAAGAMFLERIPRSI 469
QY 361  PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 470  PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 503

RESULT 10
US-11-077-276-8
; Sequence 8, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 8
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-8

Query Match      98.6%; Score 2003; DB 7; Length 503;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 60
Db 110  EDPGDAAQKTDTSHHDQDHTFNKIPNLAEFAFSLYRQLAQHSNSTNIFSPVSIATA 169
QY 61  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 120
Db 170  FAMLSTGKTADTHDEILEGLNFNLTOIPEAQIHEGFOELLRTLNQDPSQLQTTGNGLFL 229
QY 121  SOGLKLVDFLEVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 180
Db 230  SEGKLVDKFLVDKVLKLYHSEAFVNFPGDTEAKQINDYVEKGTQCKIVDLVKELDRDT 289
QY 181  VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCKKLSWVL 240
Db 290  VFALVNYIFFKGKWERPFVKDTEEDFHVQDQVTVTKVPMKRLGMFNIQHCKKLSWVL 349
QY 241  LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 300
Db 350  LMKYLGNAITAIFFLPDEGKLOHLENELTHDIIITKFLNEDRRRSASLHLPKLSITGTGYDLK 409
QY 301  SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIIDEKGTAAAGAMFLERIPRSI 360
Db 410  SVLGQIGITKVFNSGADLSGVTTEAPLKLKSAVHKAVLTIIDEKGTAAAGAMFLERIPRSI 469
QY 361  PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 394
Db 470  PPEVKFNKPFVFLMIEQNTKSPFLFMGKVNPQTOK 503

RESULT 11
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US-11-077-276-16
; Sequence 16, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; PRIOR FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 16
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-16

Query Match
Best Local Similarity 98.6%; Score 2003; DB 7; Length 503;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 129 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLISGTTKADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 189 FAMLISGTTKADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 249 SEGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTTVKVPMKRLGFMFNIOHCKKLSWWL 240
DB 309 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTTVKVPMKRLGFMFNIOHCKKLSWWL 368
QY 241 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 369 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 428
QY 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 429 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 488
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 489 PPEVKENKPFVFLMIEQNTKSPFLFMGKVNPQTK 522

RESULT 13
PCT-US05-07959-20
; Sequence 20, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-20

Query Match
Best Local Similarity 98.6%; Score 2003; DB 1; Length 522;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 2 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 61
QY 61 FAMLISGTTKADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 62 FAMLISGTTKADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 121
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 122 SEGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 181
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTTVKVPMKRLGFMFNIOHCKKLSWWL 240
DB 182 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTTVKVPMKRLGFMFNIOHCKKLSWWL 241
QY 241 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 302 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 361
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 362 PPEVKENKPFVFLMIEQNTKSPFLFMGKVNPQTK 395

RESULT 12
PCT-US05-07959-14
; Sequence 14, Application PC/TUS0507959
; GENERAL INFORMATION:
; APPLICANT: Arriva Pharmaceuticals, Inc.
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020 PCT
; CURRENT APPLICATION NUMBER: PCT/US05/07959
; PRIOR FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 14
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-07959-14

Query Match
Best Local Similarity 98.6%; Score 2003; DB 1; Length 522;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 60
DB 129 EDPOGDAAKTDTSHHDQDHPFNKITPNLAFAFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLISGTTKADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
DB 189 FAMLISGTTKADTHDEILEGNFNLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SQGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
DB 249 SEGLKLVDFLEVDVKLYHSEAFVNFVFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTTVKVPMKRLGFMFNIOHCKKLSWWL 240
DB 309 VFALVNYIFFKGKWERPFVKDTEEDFHVDTQVTTVKVPMKRLGFMFNIOHCKKLSWWL 368
QY 241 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 300
DB 369 LMKYLGNAITAIFFLPDDEGKLOHLENELTHDIIITKFLNEDRRSASLHLPKLSITGTGYDLK 428
QY 301 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPRSI 360
DB 429 SVLGQGITKTVFSNGADLSGVTEEAAPLKLKSAVHKAVLTIDKGTAAAGAMFLERIPMSI 488
QY 361 PPEVKENKPFVFLMIEQNTKSPFLFMGKVNPQTK 394
DB 489 PPEVKENKPFVFLMIEQNTKSPFLFMGKVNPQTK 522
```

Db 242 LMKYLGNAITFPLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 301
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 360
Db 302 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 361
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 362 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 395

RESULT 14

US-11-077-276-14
; Sequence 14, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 14
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-14

Query Match 98.6%; Score 2003; DB 7; Length 522;
Best Local Similarity 98.5%; Pred. No. 1.8e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQKTDTSHHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 129 EDPOGDAQKTDTSHHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 188
QY 61 FAMLISLGTAKDTHDEILEGLNENLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 189 FAMLISLGTAKDTHDEILEGLNENLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 248
QY 121 SOGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 249 SEGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 308
QY 181 VFALVNYIIFPKGKWERPPEVKDTEBEDFHVDDVTTVKVPMKRLGFMNIOHCKKLSWVL 240
Db 309 VFALVNYIIFPKGKWERPPEVKDTEBEDFHVDDVTTVKVPMKRLGFMNIOHCKKLSWVL 368
QY 241 LMKYLGNAITFPLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 369 LMKYLGNAITFPLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 428
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 360
Db 429 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 488
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 489 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 522

RESULT 15

US-11-077-276-20
; Sequence 20, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip J. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY

; TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
; FILE REFERENCE: 39042-0020
; CURRENT APPLICATION NUMBER: US/11/077,276
; CURRENT FILING DATE: 2005-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/551,856
; PRIOR FILING DATE: 2004-03-09
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-077-276-20

Query Match 98.6%; Score 2003; DB 7; Length 522;
Best Local Similarity 98.5%; Pred. No. 1.8e-149;
Matches 388; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 EDPOGDAQKTDTSHHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 60
Db 2 EDPOGDAQKTDTSHHDQDHPFNKITPNLAEPFSLYRQLAHQSNSTNIFPSPVSIATA 61
QY 61 FAMLISLGTAKDTHDEILEGLNENLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 120
Db 62 FAMLISLGTAKDTHDEILEGLNENLTOIPEAQIHEGFQELLRTLNQDPSQLQTTGNGLFL 121
QY 121 SOGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 180
Db 122 SEGLKLVDFLEVDVKLYHSEAFVTNFGDTEQAQKQINDYVEKGTQGIKIVDLVKELDRDT 181
QY 181 VFALVNYIIFPKGKWERPPEVKDTEBEDFHVDDVTTVKVPMKRLGFMNIOHCKKLSWVL 240
Db 182 VFALVNYIIFPKGKWERPPEVKDTEBEDFHVDDVTTVKVPMKRLGFMNIOHCKKLSWVL 241
QY 241 LMKYLGNAITFPLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 300
Db 242 LMKYLGNAITFPLPDEGKQLHLENELTHDIIITKFLNEDRRSASLHLPKLSITGYDLK 301
QY 301 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 360
Db 302 SVLGQIGITKVFSGADLSGVTEAPLKLKSKAVHKAVLTIDEKGTAAAGMFLERIPRSI 361
QY 361 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 394
Db 362 PPEVKFNKPFVFLMIEQNTKSPFLFMGKVVNPTQK 395

Search completed: June 20, 2005, 19:56:55

Job time : 67 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 16:01:11 ; Search time 23 Seconds
(without alignments)
16.733 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 RIPR 4

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	57.1	4	2 A02147	phagocytosis-stimu
2	10	47.6	4	2 I54357	schwannomin - mous
3	8	38.1	3	3 I78890	tyrosine protein k
4	7	33.3	3	3 RHSH	thyroliberin - she
5	7	33.3	3	3 A92971	thyroliberin - eas
6	7	33.3	3	3 RHTD	thyroliberin - Bom
7	7	33.3	3	3 A43391	TRH-like tripeptid
8	7	33.3	3	3 RHPT	thyroliberin - pig
9	7	33.3	3	3 A33802	thyrotropin-releas
10	7	33.3	4	2 S53508	starvation-induced
11	7	33.3	4	2 A34626	RPCH-related neuro
12	7	33.3	4	2 I51049	metallothionein-A
13	7	33.3	4	2 PT0240	Ig heavy chain CRD
14	7	33.3	4	2 PL0140	carbon-monoxide de
15	7	33.3	4	2 S17255	ribosomal protein
16	7	33.3	4	2 PT0675	T-cell receptor be
17	7	33.3	4	2 PT0721	T-cell receptor be
18	7	33.3	4	2 A32039	tyrosine-melanocyt
19	6	28.6	4	2 I40804	endoglucanase F -
20	5	23.8	3	3 A22565	R-phycocerythrin al
21	5	23.8	3	3 PQ0010	angiotensin-conver
22	5	23.8	4	1 ECXAA	antho-RFamide neur
23	5	23.8	4	2 D41654	hypothetical prote
24	5	23.8	4	2 I40870	phospholipase C (B
25	5	23.8	4	2 A25844	antho-RF amide neu
26	5	23.8	4	2 I61883	protamine p1 - oxa
27	5	23.8	4	2 S47552	ubiquitin - rat
28	5	23.8	4	2 I37013	protamine p1 - Cer
29	5	23.8	4	2 I84439	protamine p1 - sav

30	5	23.8	4	2 A35779	neuropeptide Antho
31	5	23.8	4	2 A60418	FMRFamide - polych
32	5	23.8	4	2 ECNK	cardioexcitatory n
33	4	19.0	4	2 A61300	22K superhelical D
34	4	19.0	4	2 T46627	hypothetical prote
35	4	19.0	4	2 A27897	glucan 1,4-alpha-g
36	4	19.0	4	2 E44823	synptosomal-assoc
37	4	19.0	4	2 S09478	globulin IV alpha
38	4	19.0	4	2 PT0271	Ig heavy chain CRD
39	4	19.0	4	2 PT0633	T-cell receptor be
40	4	19.0	4	2 PT0551	T-cell receptor be
41	4	19.0	4	2 PT0697	phenol 2-monooxyge
42	3	14.3	4	2 A37832	cell surface adhes
43	3	14.3	4	2 B43848	hypothetical prote
44	3	14.3	4	2 I40505	hypothetical prote
45	3	14.3	4	2 T30569	COI intron 16 prot
46	3	14.3	4	2 I38888	hypothetical prote
47	3	14.3	4	2 A40135	branched-chain-ami
48	2	9.5	3	3 S13894	histidinol dehydro
49	2	9.5	3	3 E37196	bradykinin-potent
50	2	9.5	3	3 F37196	bradykinin-potent
51	2	9.5	3	3 T13892	cytochrome-c oxida
52	2	9.5	3	3 GKHU	growth-modulating
53	2	9.5	3	3 A60898	bursin - chicken
54	2	9.5	4	2 S18401	thyroglobulin - do
55	2	9.5	4	2 A48360	gamma subunit of P
56	2	9.5	4	2 S39390	myosin-light-chain
57	2	9.5	4	2 A53284	T-cell receptor be
58	2	9.5	4	2 A26209	protein-glutamine
59	2	9.5	4	2 PL0146	carbon-monoxide de
60	2	9.5	4	2 JQ1273	neuropeptide Antho
61	2	9.5	4	2 PT0645	T-cell receptor be
62	2	9.5	4	2 PT0534	T-cell receptor be
63	1	4.8	3	3 I50412	gene p20K protein
64	1	4.8	3	3 PT0578	T-cell receptor be
65	1	4.8	3	3 A23751	spinal cord peptid
66	1	4.8	3	3 B23751	spinal cord peptid
67	1	4.8	4	2 S43014	hypothetical prote
68	1	4.8	4	2 I57745	D-mannosate hydrol
69	0	0.0	3	3 PT0636	T-cell receptor be
70	0	0.0	3	3 PT0571	T-cell receptor be
71	0	0.0	3	3 PT0622	T-cell receptor be
72	0	0.0	3	3 S68328	blood cell protein
73	0	0.0	4	2 A41890	protein D - Escher
74	0	0.0	4	2 S43959	Ig mu chain V regi
75	0	0.0	4	2 B53284	T-cell receptor be
76	0	0.0	4	2 S55238	pallidipin - aasas
77	0	0.0	4	2 I40697	biotin A - Citroba
78	0	0.0	4	2 A32480	achatin-I - Giant
79	0	0.0	4	2 PT0696	T-cell receptor be
80	0	0.0	4	2 PT0711	T-cell receptor be
81	0	0.0	4	2 PT0661	T-cell receptor be
82	0	0.0	4	2 PT0712	T-cell receptor be
83	0	0.0	4	2 PT0698	T-cell receptor be
84	0	0.0	4	2 PT0677	T-cell receptor be
85	0	0.0	4	2 PT0706	T-cell receptor be
86	0	0.0	4	2 PT0566	T-cell receptor be

ALIGNMENTS

RESULT 1

A02147
phagocytosis-stimulating peptide (tuftsin) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A02147
R:Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A>Title: The characteristics, isolation and synthesis of the phagocytosis stimulating pei
A:Reference number: A02147; MUID:72187087; PMID:4112769
A:Accession: A02147

A:Molecule type: protein
A:Residues: 1-4 <NIS>
A:Cross-references: UNIPROT:P01858
A:Note: a peptide having the same structure, physical properties, and biological activities as thyroliberin - sheep
R:Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3386-3392, 1967
A:Reference number: A37502; PMID:68091045; PMID:4169272
A:Contents: annotation; immunoglobulin class
C:Comment: An IGG (called leukokinin) binds reversibly to the cell membrane of neutrophils. It is essential for maximum stimulation of the phagocytic activity of neutrophils.
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 57.1%; Score 12; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 4
||
Db 3 P 4

RESULT 2
I54357
schwannomin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C:Accession: I54357
R:Huyhn, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are controlled by a 5' upstream enhancer
A:Reference number: I54357; PMID:95072570; PMID:7981675
A:Accession: I54357
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-4 <RES>
A:Cross-references: GB:L28838; NID:G454836; PIDN:AAA57150.1; PID:G601923
C:Genetics:
A:Gene: NF2

Query Match 47.6%; Score 10; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IP 3
:|
Db 1 VP 2

RESULT 3
I78890
tyrosine protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I78890
R:Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C.
Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ntK, a csk-related tyrosine protein kinase
A:Reference number: I58407; PMID:95060800; PMID:7970703
A:Accession: I78890
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:L33339; NID:G609536; PIDN:AAA64432.1; PID:G609538
C:Genetics:
A:Gene: p52ntk

Query Match 38.1%; Score 8; DB 3; Length 3;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IP 3
:|
Db 1 MP 2

RESULT 4

RHSHT

thyroliberin - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A93750; A01415
R:Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A:Title: The elucidation of the primary structure of the hypothalamic thyroïd stimulating hormone

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 5
A92971
thyroliberin - eastern newt (tentative sequence)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A92971; A01415
R:Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 471-478, 1974
A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 6
RHTDIO
thyroliberin - Bombina orientalis
C:Species: Bombina orientalis
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C:Accession: A90919; A01415
R:Yasuhara, T.; Nakajima, T.

Query Match 33.3%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

Chem. Pharm. Bull. 23, 3301-3303, 1975

A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.

A;Reference number: A90919; MUID:76138399; PMID:815011

A;Accession: A90919

A;Molecule type: protein

A;Residues: 1-3 <VAS>

A;Cross-references: UNIPROT:P01151

C;Superfamily: thyroliberin

C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 7

A43391

TRH-like tripeptide - alfalfa

C;Species: Medicago sativa (alfalfa)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: A43391

R;Lackey, D.B.

J. Biol. Chem. 267, 17508-17511, 1992

A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglu-

A;Reference number: A43391; MUID:92388092; PMID:1517203

A;Accession: A43391

A;Molecule type: protein

A;Residues: 1-3 <LAC>

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 8

RHPGT

thyroliberin - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004

C;Accession: A01415

R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.

Biochemistry 9, 1103-1106, 1970

A;Title: Structure of porcine thyrotropin releasing hormone.

A;Reference number: A90560; MUID:70136150; PMID:4984938

A;Accession: A01415

A;Molecule type: protein

A;Residues: 1-3 <NAI>

R;Boier, J.; Enzmann, F.; Folkers, K.; Bowers, C.Y.; Schally, A.V.

Biochem. Biophys. Res. Commun. 37, 705-710, 1969

A;Title: The identity of chemical and hormonal properties of the thyrotropin releasing h

A;Reference number: A90167; MUID:70039904; PMID:4982117

A;Contents: annotation

A;Note: biological activities and Rf values (in 17 chromatographic systems) of the synth

C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 9

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004

C;Accession: A33802

R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.

J. Biol. Chem. 264, 7788-7791, 1989

A;Title: A novel peptide, pyroglutamylglutamyproline amide, in the rabbit prostate comp.

A;Reference number: A33802; MUID:89255196; PMID:2498305

A;Accession: A33802

A;Molecule type: protein

A;Residues: 1-3 <COC>

C;Keywords: amidated carboxyl end; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 7; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 3 P 3

RESULT 10

S53508

starvation-induced ribonuclease - tomato

C;Species: Lycopersicon esculentum (tomato)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999

C;Accession: S53508

R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.

Plant Mol. Biol. 27, 477-485, 1995

A;Title: cDNA structure and regulatory properties of a family of starvation-induced ribo

A;Reference number: S53506; MUID:95201242; PMID:7894013

A;Accession: S53508

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KOE>

Query Match 33.3%; Score 7; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3

DB 2 P 2

RESULT 11

A34626

RPCH-related neuropeptide - ferruginous spindle

C;Species: Fusinus ferrugineus (ferruginous spindle)

C;Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993

C;Accession: A34626

R;Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;

Biochem. Biophys. Res. Commun. 167, 273-279, 1990

A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.

A;Reference number: A34626; MUID:90179762; PMID:2310394

A;Accession: A34626

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-4 <KUR>

C;Keywords: neuropeptide

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 2 P 2

RESULT 12
I51049
metallothionein-A - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51049
R:Olsson, P.E.; Kling, P.; Erkel, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss) metallothionein-A
A:Reference number: I51049; MUID:95324545; PMID:7601121
A:Accession: I51049
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-4 <OLS>
A:Cross-references: EMBL:X80181; NID:g1019799; PIDN:CAA56466.1; PID:g4379328

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 13
PT0240
IG heavy chain CRD3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 2 P 2

RESULT 14
PL0140
carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydohydrogena
C:Species: Pseudomonas carboxydohydrogena
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: PL0140
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop
A:Reference number: PL0138; MUID:90055678; PMID:2818128
A:Accession: PL0140
A:Molecule type: protein
A:Residues: 1-4 <KRA>
A:Cross-references: UNIPROT:P19916

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

RESULT 15
S17255
ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae) (f
C:Species: Saccharomyces cerevisiae
A:Variety: strain 07173
C>Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C:Accession: S17255
R:Grohmann, L.; Graack, H.R.; Kruft, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 284, 51-56, 1991
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from y
A:Reference number: S17255; MUID:91285106; PMID:2060626
A:Accession: S17255
A:Molecule type: protein
A:Residues: 1-4 <GRO>
A:Cross-references: UNIPROT:P36515
C:Comment: A coding region for this protein could not be identified in the genome of Sac
C:Genetics:
A:Genome: nuclear
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

Search completed: June 20, 2005, 16:34:35
Job time : 24 secs

C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
C;Keywords: oxidoreductase

Query Match 33.3%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 20, 2005, 15:59:16 ; Search time 109.5 Seconds
(without alignments)
18.706 Million cell updates/sec

Title: US-09-885-914B-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	12	57.1	4	1 TUFT_HUMAN	P01858 homo sapien
2	9	42.9	4	1 FYRI_ANCEL	P58706 anthopleura
3	7	33.3	3	1 THYL_BOMOR	P62970 bombina ori
4	7	33.3	3	1 THYL_NOTVI	P62971 notophthalm
5	7	33.3	3	1 THYL_PIG	P62968 sus scrofa
6	7	33.3	3	1 THYL_SHEEP	P62969 ovis aries
7	7	33.3	4	1 DCML_PSECH	P19916 pseudomonas
8	7	33.3	4	1 YLMI_YEAST	P36515 saccharomyc
9	7	33.3	4	2 Q16047	Q16047 homo sapien
10	5	23.8	4	1 FAR3_HIRME	P42562 hirudo medi
11	5	23.8	4	1 FLRF_HIRME	P42563 hirudo medi
12	5	23.8	4	1 FLRF_HIRME	P42561 hirudo medi
13	5	23.8	4	1 FLRF_ANCEL	P58707 anthopleura
14	5	23.8	4	1 FMRE_MACNI	P01162 macrocallis
15	4	19.0	3	1 LUXE_VIBFI	P24272 vibrio fisc
16	4	19.0	4	1 ILME_SEPOF	P83568 sepio offic
17	3	14.3	4	1 E0SI_HUMAN	P02731 homo sapien
18	3	14.3	4	2 Q08433	Q08433 rattus sp.
19	2	9.5	3	1 GRWM_HUMAN	P01157 homo sapien
20	2	9.5	4	1 DCMS_PSECH	P19918 pseudomonas
21	2	9.5	4	1 PFKA_ANCEL	P58705 anthopleura
22	2	9.5	4	2 Q96A70	Q96A70 homo sapien
23	0	0.0	2	1 GWA_SEPOF	P83570 sepio offic
24	0	0.0	4	1 ACHI_ACHFU	P35904 achatina fu
25	0	0.0	4	1 OCP1_OCTMI	P58648 octopus min
26	0	0.0	4	1 OCP3_OCTMI	P58649 octopus min

ALIGNMENTS

```
RESULT 1
TUFT_HUMAN
ID TUFT_HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Phagocytosis-stimulating peptide (tuftsein).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsein.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -I- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the
cell membrane of neutrophils in the blood. Leucokininase on the
membrane releases the active peptide tuftsein from the gamma chain.
CC Tuftsein is essential for maximum stimulation of the phagocytic
activity of neutrophils.
CC PIR; A02147; A02147.
DR MIM; 191150;
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006909; P:phagocytosis; NAS.
KW Direct protein sequencing.
SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 57.1%; Score 12; DB 1; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PR 4
Db 3 PR 4

RESULT 2
FYRI_ANCEL
ID FYRI_ANCEL STANDARD; PRT; 4 AA.
AC P58706;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Antho-Riamide I [Contains: Antho-Riamide II].
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
OC Nymphaeae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110;
RN [1]
RP SEQUENCE.
RX MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-2;
RA Nthacker H.-P., Rinehart K.L. Jr., McFarlane I.D.;
RA Grimmelikhuijzen C.J.P.;
RT "Isolation of two novel neuropeptides from sea anemones: the unusual,
biologically active L-3-phenylalanyl-Tyr-Arg-Ile-NH2 and its des-
phenylalanyl fragment Tyr-Arg-Ile-NH2.";
RL Peptides 12:1165-1173(1991).
RN [2]
RP FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;
```

RT "The expansion behaviour of sea anemones may be coordinated by two
 RL inhibitory neuropeptides, Antho-Kamide and Antho-Ramide.";
 RL Proc R. Soc. Lond. B, Biol. Sci. 253:183-188(1993).
 CC -1- FUNCTION: Inhibits spontaneous contractions in several muscle
 CC groups. May be involved in the expansion phase of feeding
 CC behaviour in sea anemones.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron specific.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT CHAIN 1 4 Antho-Ramide I.
 FT CHAIN 2 4 Antho-Kamide II.
 FT MOD_RES 1 1 3-phenyllactic acid.
 FT MOD_RES 4 4 Isoleucine amide.
 SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match 42.9%; Score 9; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RI 2
 ||
 3 RI 4

Db

RESULT 3

THYL_BOMOR STANDARD; PRT; 3 AA.

AC P62970; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 OS Bombina orientalis (Oriental fire-bellied toad).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
 OX NCBI_TaxID=8346;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Skin;
 RX MEDLINE=76138399; PubMed=815011;
 RA Yasuhara T., Nakajima T.;
 RT "Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
 RL Chem. Pharm. Bull. 23:3301-3303(1975).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR; A90919; RHTDTC.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 3 P 3

Db

RESULT 4

THYL_NOTVI STANDARD; PRT; 3 AA.

AC P62971; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).

OS Notoptthalmus viridescens (Eastern newt) (Triturus viridescens).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae;
 OC Notoptthalmus.
 OX NCBI_TaxID=8316;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Brain;
 RX MEDLINE=75035605; PubMed=4214528;
 RA Grimm-Joergensen Y., McKelvy J.P.;
 RT "Biosynthesis of thyrotropin releasing factor by newt (Triturus
 RT viridescens) brain in vitro. Isolation and characterization of
 RT thyrotropin releasing factor.";
 RL J. Neurochem. 23:471-478(1974).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR; A92971; A92971.
 KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
 |
 3 P 3

Db

RESULT 5

THYL_PIG STANDARD; PRT; 3 AA.

AC P62968; P01151;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin
 DE releasing factor) (TSH-releasing factor) (Protirelin).
 GN Name=TRH;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Hypothalamus;
 RX MEDLINE=70136150; PubMed=4984938;
 RA Nair R.M.G., Barrett J.F., Bowers C.Y., Schally A.V.;
 RT "Structure of porcine thyrotropin releasing hormone.";
 RL Biochemistry 9:1103-1106(1970).
 RN [2]
 RP SYNTHESIS.

RC MEDLINE=70039904; PubMed=4982117;
 RA Boler J., Enzmann F., Folkers K., Bowers C.Y., Schally A.V.;
 RT "The identity of chemical and hormonal properties of the thyrotropin
 RT releasing hormone and pyroglutamyl-histidyl-proline amide.";
 RL Biochem. Biophys. Res. Commun. 37:705-710(1969).
 CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH
 CC in the anterior pituitary gland and as a neurotransmitter/
 CC neuromodulator in the central and peripheral nervous systems.
 CC -1- SUBCELLULAR LOCATION: Secreted.

KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
 FT MOD_RES 3 3 Proline amide.
 SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 6

THYL_SHEEP STANDARD; PRT; 3 AA.
AC P62969; P01151;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor) (Protirelin).
GN Names-TRH;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Hypothalamus;
RA Desiderio D.M. Jr., Burgess R., Dunn T.F., Vale W., Guillemin R., Ward D.N.;
RT "The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass spectrometry.";
RL Org. Mass Spectrom. 5:221-228(1971).
RN [2]
RP SYNTHESIS.
RX MEDLINE=70163386; PubMed=4985794;
RA Burgess R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W., Guillemin R.;
RT "Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.";
RL Nature 226:321-325(1970).
CC -1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems.
CC -1- SUBCELLULAR LOCATION: Secreted.
DR PIR; A93750; RSHST.
KW Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 3 3 Proline amide.
SQ SEQUENCE 3 AA; 380 MW; 7761F6B000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 3;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 3 P 3

RESULT 7

DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO dehydrogenase subunit L) (CO-DH L) (Fragment).
GN Names=cutL;
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.

RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in carboxydophilic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
CC -1- COFACTOR: Binds 1 copper(I) ion, 1 molybdenum(VI) ion and 1 molybdopterin cytosine dinucleotide (MCD) per subunit.
CC -1- SUBUNIT: Heterotrimer consisting of a large, a medium and a small subunit.
DR PIR; P01040; PLO140.
KW Direct protein sequencing; Molybdenum; Oxidoreductase.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

RESULT 8

YLM1_YEAST STANDARD; PRT; 4 AA.
AC P365I5;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment).
GN Name=YmL1;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE.
RX MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
RA Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S., Kitakawa M.;
RT "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
RL FEBS Lett. 284:51-56(1991).
CC -1- FUNCTION: Putative component of the large subunit of mitochondrial ribosome.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
DR PIR; S17255; S17255.
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D000000000 CRC64;

Query Match 33.3%; Score 7; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 P 3
|
Db 4 P 4

RESULT 9

Q16047 PRELIMINARY; PRT; 4 AA.
AC Q16047;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Interleukin 2 receptor alpha-subunit (fragment).
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92062171; PubMed=1840490;
 RA Marcken L., Moras V., Henon L., Lionne B., Bousseau A.,
 RA Dautry-Varsat A., Collins M., Mayaux J.F.;
 RT "An exon 5-deleted mRNA encodes a functional interleukin 2 receptor
 alpha-subunit.";
 RL Biochem. Biophys. Res. Commun. 180:1390-1395 (1991).
 DR ENBL; S64248; AAB20279.1; -;
 DR HSP; P01112; 1PLL.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
 DR InterPro; IPR001806; Ras-Grb2 binding.
 DR PRINTS; PR00449; RASTRNSFRMG.
 KW Receptor.
 FT NON TER.
 SQ SEQUENCE 4 AA; 525 MW; 69CAB769A0000000 CRC64;
 Query Match 33.3%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 P 3
 Db 2 P 2
 RESULT 10
 FAR3_HIRME STANDARD; PRT; 4 AA.
 AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide YLRF-amide.
 OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908 (1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 R 1
 Db 3 R 3
 RESULT 11
 FAR4_HIRME STANDARD; PRT; 4 AA.
 AC P42563;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRFamide-like neuropeptide YMRP-amide.

OS Hirudo medicinalis (Medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908 (1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 R 1
 Db 3 R 3
 RESULT 12
 FLRF_HIRME STANDARD; PRT; 4 AA.
 AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FLRFamide.
 OS Hirudo medicinalis (Medicinal leech), and
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea;
 OC Arhynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421, 27815;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908 (1991).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 582 MW; 69D40729A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 R 1
 Db 3 R 3
 RESULT 13
 FLRN_ANTEL STANDARD; PRT; 4 AA.
 ID FLRN_ANTEL

AC P58707;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antho-RNAmide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nyanthaeae; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;
 RN
 RN SEQUENCE, AND MASS SPECTROMETRY.
 RX MEDLINE=90319122; PubMed=1973541;
 RA Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
 RA Reinscheid R.K., Notherhack H.-P., Staley A.L.,
 RT "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH₂ (Antho-RNAmide), a sea
 RT anemone neuropeptide containing an unusual amino-terminal blocking
 RT group.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414 (1990).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Neuron specific.
 CC -1- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
 DR PIR; A35779;
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 1 1 3-phenyllactic acid.
 FT MOD_RES 4 4 Asparagine amide.
 SQ SEQUENCE 4 AA; 549 MW; 64540729A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 DB 3 R 3
 RESULT 14
 FMRP_MACNI STANDARD; PRT; 4 AA.
 AC P01162;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE FMRamide (Peak C) (Cardioexcitatory neuropeptide).
 OS Macrocallista nimbosa (Sun-ray clam),
 OS Nereis virens (Sandworm),
 OS Helisoma trivolvis (Medicinal leech), and
 OS Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroidea;
 OC Veneroidea; Veneridae; Macrocallista.
 OX NCBI_TaxID=6594, 6353, 6421, 27815;
 RN
 RN SEQUENCE, AND SYNTHESIS.
 RC SPECIES=M.nimbosa; TISSUE=Cerebral pedal, and Visceral ganglion;
 RX MEDLINE=77215956; PubMed=877582;
 RA Price D.A., Greenberg M.J.;
 RT "Structure of a molluscan cardioexcitatory neuropeptide.";
 RL Science 197:670-671 (1977).
 RN
 RN SEQUENCE, AND CHARACTERIZATION.
 RC SPECIES=M.nimbosa; TISSUE=Ganglion;
 RX MEDLINE=78012038; PubMed=909875;
 RA Price D.A., Greenberg M.J.;
 RT "Purification and characterization of a cardioexcitatory neuropeptide
 RT from the central ganglia of a bivalve mollusc.";
 RL Prep. Biochem. 7:261-281 (1977).
 RN
 RN SEQUENCE.
 RC SPECIES=N.virens;
 RX MEDLINE=90259866; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;
 RA Krajniak K.G., Price D.A.;
 RT "Authentic FMRamide is present in the polychaete Nereis virens.";
 RL Peptides 11:75-77 (1990).

RN
 RN SEQUENCE.
 RC SPECIES=H.medicalinalis;
 RX MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
 RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech.";
 RL Peptides 12:897-908 (1991).
 RN
 RN SEQUENCE.
 RC SPECIES=H.trivolvis; TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRamide-related peptides from the kidney of the snail, Helisoma
 RT trivolvis.";
 RL Peptides 15:31-36 (1994).
 CC -1- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological
 CC activities include augmentation, induction, and regularization of
 CC cardiac contraction.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 DR PIR; A01426; ECKK.
 DR PIR; A60418; A60418.
 KW Amidation; Direct protein sequencing; Neuropeptide.
 FT MOD_RES 4 4 Phenylalanine amide.
 SQ SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;
 Query Match 23.8%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R 1
 DB 3 R 3
 RESULT 15
 LUXE_VIBFI STANDARD; PRT; 3 AA.
 AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-
 DE protein synthetase) (Fragment).
 GN Name=luxe;
 OS Vibrio fischeri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=668;
 RN
 RN SEQUENCE FROM N.A.
 RP MEDLINE=91072226; PubMed=2254256;
 RA Swartzman E., Kapoor S., Graham A.F., Meighen E.A.;
 RT "A new Vibrio fischeri lux gene precedes a bidirectional termination
 RT site for the lux operon.";
 RL J. Bacteriol. 172:6797-6802 (1990).
 CC -1- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It
 CC is a component of the fatty acid reductase complex responsible for
 CC converting tetradecanoic acid to the aldehyde which serves as
 CC substrate in the luciferase-catalyzed reaction.
 CC -1- CATALYTIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate +
 CC an acyl-protein thioester.
 CC -1- PATHWAY: Bioluminescent fatty acid reduction system; second step.
 CC -1- SIMILARITY: Belongs to the luxe family.
 CC
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OM protein - protein search, using sw model

Run on: June 20, 2005, 14:16:51 ; Search time 113.5 Seconds

(without alignments)
13.630 Million cell updates/sec

Title: US-09-885-914b-2

Perfect score: 21

Sequence: 1 R1PR 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 19815

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20038s:*

8: Geneseqp20048s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	100.0	4	2	AAR59927
2	21	100.0	4	2	AAY44202
3	20	95.2	4	8	ADJ57388
4	19	90.5	4	5	AU78507
5	19	90.5	4	5	AU78526
6	17	81.0	4	8	ADK42152
7	16	76.2	4	2	AAR52385
8	16	76.2	4	2	AAR52384
9	16	76.2	4	2	AAR52383
10	16	76.2	4	2	AAY44204
11	16	76.2	4	2	AAY09581
12	16	76.2	4	2	AAY09582
13	16	76.2	4	2	AAY09580
14	16	76.2	4	7	ADC13966
15	16	76.2	4	8	ADG94025
16	16	76.2	4	8	ADI46295
17	16	76.2	4	8	ADP86600
18	16	76.2	4	8	ADSI14002
19	15	71.4	4	2	AAR5261
20	15	71.4	4	2	AAR86902
21	15	71.4	4	2	AAW21760
22	15	71.4	4	2	AAW75972
23	15	71.4	4	3	AAY84384
24	15	71.4	4	3	AAB19559
25	15	71.4	4	3	AAY95742

26	15	71.4	4	4	AAR07853
27	15	71.4	4	4	AAR48691
28	15	71.4	4	5	AAB71247
29	15	71.4	4	5	AAU86935
30	15	71.4	4	5	AAU79240
31	15	71.4	4	6	ABG74124
32	15	71.4	4	6	ABP59998
33	15	71.4	4	6	ABG72040
34	15	71.4	4	6	AAR35823
35	15	71.4	4	6	ABR43318
36	15	71.4	4	6	AAR32090
37	15	71.4	4	6	ABG72334
38	15	71.4	4	6	ABR83547
39	15	71.4	4	7	ADC13980
40	15	71.4	4	8	ADG94151
41	15	71.4	4	8	ADJ46400
42	15	71.4	4	8	ADK71675
43	15	71.4	4	8	ADI46302
44	15	71.4	4	8	ADI46503
45	15	71.4	4	8	ADN48504
46	15	71.4	4	8	ADP86726
47	15	71.4	4	8	ADR38558
48	15	71.4	4	8	ADSI13999
49	15	71.4	4	8	ADSI13989
50	14	66.7	3	6	ABR43883
51	14	66.7	3	8	ADM01248
52	14	66.7	4	1	AAPI0134
53	14	66.7	4	2	AAR15327
54	14	66.7	4	2	AAR26423
55	14	66.7	4	2	AAR38137
56	14	66.7	4	2	AAR79354
57	14	66.7	4	2	AAW03144
58	14	66.7	4	2	AAW52360
59	14	66.7	4	2	AAW28140
60	14	66.7	4	2	AAW28143
61	14	66.7	4	2	AAW28142
62	14	66.7	4	2	AAW27998
63	14	66.7	4	2	AAW28141
64	14	66.7	4	2	AAW06088
65	14	66.7	4	3	AAW09557
66	14	66.7	4	3	AAW94546
67	14	66.7	4	5	AAU78864
68	14	66.7	4	5	AAE24415
69	14	66.7	4	5	AAE25916
70	14	66.7	4	5	ABG66063
71	14	66.7	4	5	ABG97617
72	14	66.7	4	5	AAO15382
73	14	66.7	4	7	ABR82527
74	14	66.7	4	7	ADC98013
75	14	66.7	4	7	ADL17647
76	14	66.7	4	8	ADG25097
77	14	66.7	4	8	ADG18987
78	14	66.7	4	8	ADK42346
79	14	66.7	4	8	ADK42347
80	14	66.7	4	8	ADQ33808
81	14	66.7	4	8	ADQ04663
82	14	66.7	4	8	ADQ04664
83	14	66.7	4	8	ADQ04507
84	14	66.7	4	8	ADQ04675
85	14	66.7	4	8	ADQ04662
86	14	66.7	4	8	ADQ04767
87	14	66.7	4	8	ADQ04687
88	14	66.7	4	8	ADQ04661
89	14	66.7	4	8	ADSI14001
90	13	61.9	4	2	AAR48072
91	13	61.9	4	2	AAR64131
92	13	61.9	4	2	AAW32851
93	13	61.9	4	2	AAW33405
94	13	61.9	4	3	ABR35836
95	13	61.9	4	4	AAU09059
96	13	61.9	4	5	ABG70627
97	13	61.9	4	6	ABP74896
98	13	61.9	4	6	AAE36043

Aae07853	Thrombin
Aab48691	Thrombin
Aab71247	Murine Ig
Aau86935	Immunoglob
Aau79240	Thrombin
Abg74124	Thrombin
Abp59998	Thrombin
Abg72040	Maltose b
Aae35823	Smac tetr
AbR43318	Thrombin
Aae32090	Expansin
Abg72334	Thrombin
AbR83547	Fusion pr
Adc13980	Rheumatol
Adg94151	Human JAM
Adj46400	Thrombin
Adk71675	Peptide c
Adi46302	Permeabil
Adi46503	Permeabil
Adn48504	M-Mulv re
Adp86726	Junctiona
Adr38558	Inhibitor
Adsi13999	Thrombin
Adsi13989	Thrombin
AbR43883	Synovial
Adm01248	Targeted
Adpi0134	Sequence
Aar15327	Tuftsia a
Aar26423	Immune en
Aar38137	Protease-
Aar79354	Human con
Aaw03144	S. aureus
Aaw52360	Beta-turn
Aay28140	Factor Xa
Aay28143	Factor Xa
Aay28142	Factor Xa
Aay27998	Factor Xa
Aay28141	Factor Xa
Aay6088	Archvilli
Aay94546	T. lanugin
Aay9557	Antimicro
Aau78864	Antimicro
Aae24415	Transport
Aae25916	Mouse and
Abg66063	Phage dip
Abg97617	Viral pep
Aao15382	Human Arf
AbR82527	Human apy
Adc98013	Signallin
Adl17647	MUPP PD27
Adg25097	Antimicro
Adg18987	Antimicro
Adk42346	Antibacte
Adk42347	Antibacte
Adq33808	Tetrapept
Adq04663	Factor XA
Adq04664	Factor XA
Adq04507	Factor XA
Adq04675	Factor XA
Adq04662	Factor XA
Adq04767	Factor XA
Adq04687	Factor XA
Adq04661	Factor XA
Adsi14001	Thrombin
Aar48072	Biologica
Aar64131	Memory-st
Aaw32851	Protectin
Aaw33405	Thrombin
Aab35836	T7 phage
Aau09059	Human thr
Abg70627	Human pro
Abp74896	Proteome
Aae36043	Cleavage

99 13 61.9 4 8 ADR49058 Caspase e
100 12 57.1 3 2 AAR30753 IGE-mast

ALIGNMENTS

RESULT 1

AAR59927 standard; peptide; 4 AA.

XX AAR59927;
XX 25-MAR-2003 (revised)
DT 14-FEB-1995 (first entry)
XX
XX Alpha 1-antitrypsin Portland residues 355-358.

XX
XX Furin endopeptidase inhibitor; variant; bacterial infection;
KW AAT Portland.
KW
XX Synthetic.

OS
XX WO9416073-A2.

PN
XX 21-JUL-1994.

PD
XX 07-JAN-1994; 94WO-US000247.

PF
XX 08-JAN-1993; 93US-00002202.

XX
XX (UYOR-) UNIV OREGON HEALTH SCI.

PA
XX Thomas G, Anderson ED, Thomas L, Hayflick JS, Nelson J;
PI Stenglen SG;

XX
XX WPI; 1994-249220/30.

XX
XX Furin endo;protease inhibitor to inhibit and treat bacterial and viral
PT infections - comprises an alpha-1 antitrypsin variant, pref. Portland.

PS
XX Disclosure; Page 29; 42pp; English.

XX
XX The sequence is that of alpha 1 antitrypsin Portland (AAT Portland)
CC residues 355-358 which is a furin endopeptidase inhibitor. The AAT
CC variant can be used to inhibit bacterial infections, esp. those caused by
CC Corynebacterium diphtheriae, Bacillus anthracis and Pseudomonas
CC aeruginosa, and to treat viral infections, esp. HIV and influenza.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db ||||
1 R1PR 4

RESULT 2

AA44202
ID AA44202 standard; protein; 4 AA.

XX
XX AAY44202;

XX 25-JAN-2000 (first entry)

XX
XX Reactive site loop of alphas-1-antitrypsin variant Portland.

XX
XX Reactive site loop; RSL; alpha-1 antitrypsin variant Portland; PDX;
KW pharmacophore; guanidino residue; peptide mimetic; bacterial toxin;

KW furin recognition site; endoproteolytic activation;
KW endolytic maturation viral protein; bacterial infection; viral infection.
XX Synthetic.
OS Homo sapiens.

XX
XX Key Location/Qualifiers

FT Misc-difference 1 /note= "wild type Ala substituted by Arg"

FT Misc-difference 4 /note= "wild type Met substituted by Arg"

XX
XX WO951624-A1.

XX
XX 14-OCT-1999.

XX
XX 08-APR-1999; 99WO-US007776.

XX
XX 08-APR-1998; 98US-0081034P.

XX
XX (UYOR-) UNIV OREGON HEALTH SCI.

XX
XX Jean F, Thomas G;

XX
XX WPI; 1999-620190/53.

XX
XX New furin endoprotease inhibitor that mimics a specific region of alpha-1
PT antitrypsin Portland mutant, for treatment and prevention of bacterial
PT and viral infection.

XX
XX Claim 1; Page 4; 108pp; English.

XX
XX The present sequence is the reactive site loop of alpha-1 antitrypsin
CC mutated variant Portland (also termed PDX). This portion of the PDX
CC protein acts as the pharmacophore necessary for biological activity. The
CC RSL forms a rigid backbone having positively-charged guanidino residues
CC of each of the Arg residues extending in space away in the same direction
CC from the rest of the PDX protein. Peptides or peptide mimetics comprising
CC this sequence inhibit bacterial toxins that are processed at a consensus
CC furin recognition site, when administered in therapeutically effective
CC amounts. Endoproteolytic activation of bacterial toxins and endolytic
CC maturation of viral proteins is blocked by the peptide and peptide
CC mimetics. This is useful in treating infections of cells by bacteria and
CC viruses. It may also be used to inhibit processing of biologically active
CC proteins

XX
SQ Sequence 4 AA;

Query Match 100.0%; Score 21; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 R1PR 4
Db ||||
1 R1PR 4

RESULT 3

ADJ57388
ID ADJ57388 standard; peptide; 4 AA.

XX
XX ADJ57388;

XX
XX 06-MAY-2004 (first entry)

XX
XX Peptide fragment of alpha-1-antitrypsin, use as convertase inhibitor.

XX
XX Convertase; inhibitor; alpha-1-antitrypsin; antiinflammatory; vulneryary;
KW ophthalmological; dermatological; nephrotropic; hepatotropic;
KW vasotropic; antiinfertility; respiratory-gen.; cardiant; CNS-gen.;
KW cerebroprotective; neuroprotective; nootropic; cytostatic; antiarthritic;
KW antiarteriosclerotic.

OS Unidentified.
 PN WO2004009113-A1.
 XX
 PD 29-JAN-2004.
 XX
 XX 23-JUL-2003; 2003WO-GB003159.
 PP
 XX 24-JUL-2002; 2002GB-00017136.
 PR
 XX (RENO-) RENOVO LTD.
 PA
 XX Ferguson MWJ, Brunner G;
 PI
 XX WPI; 2004-180270/17.
 DR
 XX
 XX Use of a convertase inhibitor in the manufacture of a medicament for
 PT reducing scarring during the healing of wounds or reducing fibrosis in
 PT the treatment of fibrotic conditions.
 PT
 XX
 PS Disclosure; Page 10; 43pp; English.
 XX
 CC The present sequence is that of a peptide fragment of alpha-1-
 CC antitrypsin. Convertase inhibitors of the invention may be derivatives of
 CC alpha-1-antitrypsin comprising this sequence. The inventors have
 CC established that convertase enzymes act, both extracellularly and
 CC intracellularly, to cause the activation of latent transforming growth
 CC factor-beta (TGF-beta) in the extracellular space at the site of a wound
 CC of a fibrotic conditions. Thus, the present invention relates to use of
 CC convertase inhibitors for the reduction of scarring during the healing of
 CC wounds, for reducing fibrosis in the treatment of fibrotic conditions,
 CC for treating wounds to prevent scar formation, for preventing scarring of
 CC the eye, nervous tissue or intestines, dermal scarring and scarring
 CC following a burn. The fibrotic condition is a fibrotic disorder such as
 CC glomerulonephritis, cirrhosis of the liver, fibrocytic disease, adhesions
 CC and restenosis (all claimed). The convertase inhibitor can also be used
 CC for the treatment of hypertrophic and keloid scars, scarring in the heart,
 CC scarring of the gut, scarring in the pelvis in the region of the
 CC fallopian tubes leading to infertility, scarring following injury to the
 CC muscles, scarring or fibrosis following injury to tendons and ligaments,
 CC which can result in serious loss of function, liver fibrosis, pulmonary
 CC fibrosis, scleroderma, myocardial hibernation, fibrosis following a stroke
 CC myocardial infarction, central nervous system fibrosis following a stroke
 CC or neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
 CC vitreoretinopathy, arthritis, arteriosclerosis and cancer.
 XX
 SQ Sequence 4 AA; .
 Query Match 95.2%; Score 20; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R1RP 4
 Db 1 RVP 4
 |||
 |||
 RESULT 4
 AAU78507
 ID AAU78507 standard; peptide; 4 AA.
 XX
 AC AAU78507;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX BACE proprotein convertase cleavage site.
 DE
 XX Alzheimer's disease; beta amyloid precursor protein; BACE;
 KW beta-site APP cleaving enzyme; nontropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 KW BACE secretase/sheddase; neurodegenerative disorder;
 KW proprotein convertase.
 XX

OS Unidentified.
 PN WO200210354-A2.
 XX
 XX 07-FEB-2002.
 PD
 XX 01-AUG-2001; 2001WO-CA001118.
 PF
 XX 01-AUG-2000; 2000CA-02313828.
 PR
 XX (RECL-) INST RECH CLINIQUES MONTREAL.
 PA
 XX Seidah NG, Chretien M, Cromlish JA;
 PI
 XX WPI; 2002-280632/32.
 DR
 XX
 XX Modulating activity of beta-site amyloid precursor protein-cleaving
 PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
 PT characterized by generation of Abeta protein, by preventing cleavage of
 PT enzyme.
 PT
 XX
 PS Disclosure; Page 19; 64pp; English.
 XX
 CC This invention relates to a novel method for modulating activity of beta-
 CC site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable of
 CC hybridising with BACE mRNA, by using a ribozyme that targets and degrades
 CC BACE secretase mRNA, with a peptide that can interfere with binding of
 CC the enzyme with BACE or using an antibody or antagonist that can function
 CC as an inhibitor of BACE secretase activation. The methods of the
 CC invention modulate the activity of BACE secretase/sheddase by preventing
 CC cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised by
 CC the generation of Abeta protein by measuring the levels of BACE C
 CC terminal cleavage products in a sample or tissue where an increase in
 CC cleavage products indicates a person at risk. The present sequence
 CC represents the BACE proprotein convertase cleavage site used to create
 CC the prosegment deletion mutants of the invention
 XX
 SQ Sequence 4 AA;
 Query Match 90.5%; Score 19; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 R1RP 4
 Db 1 RLPR 4
 |||
 |||
 RESULT 5
 AAU78526
 ID AAU78526 standard; peptide; 4 AA.
 XX
 AC AAU78526;
 XX
 XX 18-JUN-2002 (first entry)
 DT
 XX RLPR proBACE cleavage site.
 DE
 XX Alzheimer's disease; beta amyloid precursor protein; BACE;
 KW beta-site APP cleaving enzyme; nontropic; neuroprotective;
 KW beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
 KW

KW BACE secretase/sheddase; neurodegenerative disorder.
 XX Unidentified.
 OS
 PN WO200210354-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 01-AUG-2001; 2001WO-CA001118.
 XX
 PR 01-AUG-2000; 2000CA-02313828.
 XX
 PA (RECL-) INST RECH CLINIQUES MONTREAL.
 XX
 PI Seidah NG, Chretien M, Cromlish JA;
 XX WPI; 2002-280632/32.
 DR
 XX
 XX Modulating activity of beta-site amyloid precursor protein-cleaving
 PT enzyme secretase/sheddase for treatment of neurodegenerative disorder
 PT characterized by generation of Abeta protein, by preventing cleavage of
 PT enzyme.
 PS Disclosure; Page 3; 64pp; English.
 XX
 XX This invention relates to a novel method for modulating activity of beta-
 CC site amyloid precursor protein (APP)-cleaving enzyme (BACE)
 CC secretase/sheddase. Cleavage of BACE by this enzyme results in the
 CC generation of a soluble BACE which enhances the production of the
 CC amyloidogenic peptide Abeta which has been shown to be involved in the
 CC aetiology of Alzheimer's disease. Inhibition of BACE secretase can be
 CC achieved by administration of an antisense nucleotide molecule capable of
 CC hybridising with BACE mRNA, by using a ribozyme that targets and degrades
 CC BACE secretase mRNA, with a peptide that can interfere with binding of
 CC the enzyme with BACE or using an antibody or antagonist that can function
 CC as an inhibitor of BACE secretase activation. The methods of the
 CC invention modulate the activity of BACE secretase/sheddase by preventing
 CC cleavage of BACE, which is useful for the treatment of a
 CC neurodegenerative disorder characterised by the generation of Abeta
 CC protein, especially Alzheimer's disease. The invention also comprises a
 CC method for identification of an agent that can alter the ability of BACE
 CC secretase to associate with and process a known substrate, this method
 CC can be used for high throughput screening of candidate molecules. The
 CC invention also comprises a method for determining whether an individual
 CC is at risk of developing a neurodegenerative disorder characterised by
 CC the generation of Abeta protein by measuring the levels of BACE C
 CC terminal cleavage products in a sample or tissue where an increase in
 CC cleavage products indicates a person at risk. The present sequence
 CC represents the RLPR cleavage site important for probACE processing
 XX
 SQ Sequence 4 AA;
 Query Match 90.5%; Score 19; DB 5; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIPR 4
 | : | |
 Db 1 RLPR 4
 RESULT 6
 ADK42152
 ID ADK42152 standard; peptide; 4 AA.
 XX
 AC ADK42152;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Antibacterial peptide from HBP #133.
 XX
 KW Human; heparin binding protein; HBP; neutrophil elastase; antibacterial;
 KW cytokine IL-6; monocyte; bacterial infection; sepsis; septic shock;
 KW

KW disseminated intravascular coagulation; meningococcal meningitis;
 KW pneumococcal pneumonia; inflammatory response; cell apoptosis;
 KW suppressed immune system; cancer; autoimmune diseases; trauma.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016653-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 14-AUG-2003; 2003WO-DK000542.
 XX
 PR 15-AUG-2002; 2002DK-00001212.
 PR 19-AUG-2002; 2002US-0404155P.
 PR 27-JUN-2003; 2003DK-00000987.
 XX
 PA (LEUK-) LEUKETOCH AS.
 XX
 PI Djurup R, Flodgaard HJ, Norris K;
 XX WPI; 2004-257185/24.
 DR
 XX
 XX New peptides of heparin-binding protein and/or human neutrophil elastase
 PT for manufacturing a medicament for the treatment of e.g. bacterial
 PT infections, disseminated intravascular coagulation, cancer or autoimmune
 PT diseases.
 PS Claim 52; SEQ ID NO 134; 211pp; English.
 XX
 CC The invention relates to an antibacterial peptide conforming to the
 CC generic peptide sequence appearing as ADK42632, the motif being derived
 CC from analysis of the protein sequences of human heparin binding protein,
 CC hHBP, pig pHPB and human neutrophil elastase (hNLE). Also included are a
 CC vector containing the new peptide (comprising providing an expression
 CC process for producing a DNA sequence encoding one or more of the above-
 CC mentioned amino acid sequences, transforming host cells with the vector,
 CC culturing the transformed host cells and purifying the expressed peptide),
 CC and a pharmaceutical composition comprising the new peptide. The peptide
 CC is capable of inhibiting or stimulating the secretion of cytokine IL-6
 CC from monocytes. The peptides are useful in manufacturing a medicament for
 CC the treatment of Gram-negative or Gram-positive bacterial infection, such
 CC as sepsis, severe sepsis, septic shock, disseminated intravascular
 CC coagulation, meningococcal meningitis or pneumococcal pneumonia. These
 CC may also be used in manufacturing a medicament for the stimulation or
 CC inhibition of inflammatory response, for the prevention of cell
 CC apoptosis, or for the treatment of individuals having suppressed immune
 CC system, cancer, autoimmune diseases and/or trauma. The present sequence
 CC represents an antibacterial peptide of the invention derived from human
 CC HBP.
 XX
 SQ Sequence 4 AA;
 Query Match 81.0%; Score 17; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RIPR 4
 | : | |
 Db 1 RPFR 4
 RESULT 7
 AAW52385
 ID AAW52385 standard; peptide; 4 AA.
 XX
 AC AAW52385;
 XX
 DT 01-JUL-1998 (first entry)
 XX
 DE Beta-turn region used in cyclic peptide of the invention.
 XX
 KW Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy;
 KW preservative; amphipathic anti-parallel beta-sheet region; plant disease.
 KW

XX New cyclic peptide(s) with antimicrobial activity - contain amphipathic
PT beta-sheet, loop and beta-turn regions, have better activity,
PT bio-availability and protease resistance than linear analogues.
XX
PS Claim 3; Page 148; 160pp; English.
XX
CC This sequence represents a beta-turn region used in a peptide of the
CC invention. The peptides are cyclic peptides (I), which have: (a) an
CC amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and
CC a beta-turn region (TR); (b) a net positive charge at physiological pH;
CC and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad
CC spectrum antimicrobials, specifically for use against *E. coli*,
CC *Pseudomonas aeruginosa*, methicillin-resistant *Staphylococcus aureus*
CC (MRSA), vancomycin-resistant *Enterococcus faecium* and penicillin-
CC resistant *Streptococcus pneumoniae*. More generally they are active
CC against Gram-positive or -negative bacteria, fungi, yeast and protozoa.
CC Apart from clinical uses, (I) are also used as disinfectants and
CC preservatives for medical equipment, foods, cosmetics etc., also for
CC treatment of plant diseases. Compared with non-cyclised analogues (i.e.
CC tachyplesin and protegrin type peptides), (I) and are more effective,
CC with better bioavailability and/or serum half-life (increased resistance
CC to proteolysis). They are more suitable for oral administration, can be
CC used at lower doses and are unlikely to induce development of resistant
CC strains
XX
SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
Db |||||
1 RIP 3

RESULT 10
AAY44204
ID AAY44204 standard; protein; 4 AA.
XX
AC AAY44204;
XX
XX 25-JAN-2000 (first entry)
DT
DE Generic sequence-2 of the reactive site loop of Portland protein.
XX
KW Reactive site loop; RSL; alpha-1 antitrypsin variant Portland; PDX;
KW Portland protein; pharmacophore; guanidino residue; peptide mimetic;
KW bacterial toxin; furin recognition site; endoproteolytic activation;
KW endolytic maturation; viral protein; bacterial infection;
KW viral infection.
XX
OS Synthetic.
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "Any amino acid residue"
FT
XX
PN WO9951624-A1.
XX
XX 14-OCT-1999.
PD
XX
PF 08-APR-1999; 99WO-US007776.
XX
XX 08-APR-1998; 98US-0081034P.
PR
XX (UYOR-) UNIV OREGON HEALTH SCI.
PA
XX Jean P, Thomas G;
PI
XX WPI; 1999-620190/53.
DR

XX New furin endoprotease inhibitor that mimics a specific region of alpha-1
PT antitrypsin Portland mutant, for treatment and prevention of bacterial
PT and viral infection.
XX
PS Claim 1; Page 8; 108pp; English.
XX
CC The present sequence is the reactive site loop of alpha-1 antitrypsin
CC mutated variant Portland (also termed PDX). This portion of the PDX
CC protein acts as the pharmacophore necessary for biological activity. The
CC RSL forms a rigid backbone having positively-charged guanidino residues
CC from each of the Arg residues extending in space away in the same direction
CC from the rest of the PDX protein. Peptides or peptide mimetics comprising
CC this sequence inhibit bacterial toxins that are processed at a consensus
CC furin recognition site, when administered in therapeutically effective
CC amounts. Endoproteolytic activation of bacterial toxins and endolytic
CC maturation of viral proteins is blocked by the peptide and peptide
CC mimetics. This is useful in treating infections of cells by bacteria and
CC viruses. It may also be used to inhibit processing of biologically active
CC proteins
XX
SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIPR 4
Db |||||
1 RXPR 4

RESULT 11
AAY09581
ID AAY09581 standard; peptide; 4 AA.
XX
AC AAY09581;
XX
XX 21-JUL-1999 (first entry)
DT
DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:28.
XX
KW Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
KW biocidal; bacteria; yeast; Candida species; fungi; protozoa;
KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
KW penicillin-resistant *Streptococcus pneumoniae*; cosmetic.
XX
OS Synthetic.
XX
PN WO9921879-A1.
XX
XX 06-MAY-1999.
PD
XX
PF 27-OCT-1997; 97WO-US019557.
XX
PR 27-OCT-1997; 97WO-US019557.
XX
PA (INTR-) INTRABIOTICS PHARM INC.
XX
XX Chang C, Gu L, Chen J;
PI
XX WPI; 1999-312941/26.
DR
XX Antimicrobial cyclic peptides with amphiphilic beta-sheet region.
PS
XX Claim 3; Page 150; 167pp; English.
XX
CC The present invention describes cyclic peptides (I); (i) comprising an
CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B), and a
CC beta-turn (C); (ii) having net positive charge at physiological pH; and
CC (iii) including at least one basic amino acid (aa) in (B) or (C).
CC

CC AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically
 CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
 CC antimicrobials (biostatic or biocidal), effective against bacteria, yeast
 CC (e.g. *Candida* species), fungi and protozoa. Particularly they are used to
 CC control *Escherichia coli*, *Pseudomonas aeruginosa*, vancomycin-resistant
 CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with
 CC linear analogues, (I) are more effective with better bioavailability
 CC and/or serum half-life (better resistance to proteolysis, allowing lower
 CC doses and making them more suitable for oral delivery). Since (I) are
 CC structurally related to naturally occurring antimicrobial peptides, they
 CC are less likely to induce development of resistant strains
 XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
 Db |||
 1 RIP 3

RESULT 12
 AAY09582
 ID AAY09582 standard; peptide; 4 AA.
 AC AAY09582;

DT 21-JUL-1999 (first entry)
 DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:29.

XX
 KW Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
 KW biocidal; bacteria; yeast; *Candida* species; fungi; protozoa;
 KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
 KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
 KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
 KW penicillin-resistant *Streptococcus pneumoniae*; cosmetic.
 XX
 OS Synthetic.
 XX
 PN WO9921879-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 27-OCT-1997; 97WO-US019557.
 XX
 PR 27-OCT-1997; 97WO-US019557.
 XX
 PA (INTR-) INTRABIOTICS PHARM INC.
 XX
 PI Chang C, Gu L, Chen J;
 XX
 DR WPI; 1999-312941/26.
 XX
 PT Antimicrobial cyclic peptides with amphiphilic beta-sheet region.
 XX
 PS Claim 3; Page 150; 167pp; English.

XX The present invention describes cyclic peptides (I): (i) comprising an
 CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a
 CC beta-turn (C); (ii) having net positive charge at physiological pH; and
 CC (iii) including at least one basic amino acid (aa) in (B) or (C).
 CC AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically
 CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
 CC antimicrobials (biostatic or biocidal), effective against bacteria, yeast
 CC (e.g. *Candida* species), fungi and protozoa. Particularly they are used to
 CC control *Escherichia coli*, *Pseudomonas aeruginosa*, vancomycin-resistant
 CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with

CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with
 CC linear analogues, (I) are more effective with better bioavailability
 CC and/or serum half-life (better resistance to proteolysis, allowing lower
 CC doses and making them more suitable for oral delivery). Since (I) are
 CC structurally related to naturally occurring antimicrobial peptides, they
 CC are less likely to induce development of resistant strains
 XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIP 3
 Db |||
 1 RIP 3

RESULT 13
 AAY09580
 ID AAY09580 standard; peptide; 4 AA.
 AC AAY09580;

DT 21-JUL-1999 (first entry)
 DE Antimicrobial cyclic peptide beta-turn region SEQ ID NO:27.

XX
 KW Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
 KW biocidal; bacteria; yeast; *Candida* species; fungi; protozoa;
 KW *Escherichia coli*; *Pseudomonas aeruginosa*; infection; preservative;
 KW vancomycin-resistant *Enterococcus faecium*; disinfectant; food;
 KW methicillin-resistant *Staphylococcus aureus*; medical equipment;
 KW penicillin-resistant *Streptococcus pneumoniae*; cosmetic.
 XX
 OS Synthetic.
 XX
 PN WO9921879-A1.
 XX
 PD 06-MAY-1999.
 XX
 PF 27-OCT-1997; 97WO-US019557.
 XX
 PR 27-OCT-1997; 97WO-US019557.
 XX
 PA (INTR-) INTRABIOTICS PHARM INC.
 XX
 PI Chang C, Gu L, Chen J;
 XX
 DR WPI; 1999-312941/26.
 XX
 PT Antimicrobial cyclic peptides with amphiphilic beta-sheet region.
 XX
 PS Claim 3; Page 150; 167pp; English.

XX The present invention describes cyclic peptides (I): (i) comprising an
 CC amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a
 CC beta-turn (C); (ii) having net positive charge at physiological pH; and
 CC (iii) including at least one basic amino acid (aa) in (B) or (C).
 CC AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically
 CC claimed cyclic peptides and peptide segments. (I) are broad-spectrum
 CC antimicrobials (biostatic or biocidal), effective against bacteria, yeast
 CC (e.g. *Candida* species), fungi and protozoa. Particularly they are used to
 CC control *Escherichia coli*, *Pseudomonas aeruginosa*, vancomycin-resistant
 CC *Enterococcus faecium*, methicillin-resistant *Staphylococcus aureus* and
 CC penicillin-resistant *Streptococcus pneumoniae*. (A) are used to treat or
 CC prevent infections, in animals or plants, also as preservatives and
 CC disinfectants for medical equipment, foods, cosmetics, optionally as
 CC mixtures or in combination with other antimicrobials. Compared with

CC linear analogues, (I) are more effective with better bioavailability
 CC and/or serum half-life (better resistance to proteolysis, allowing lower
 CC doses and making them more suitable for oral delivery). Since (I) are
 CC structurally related to naturally occurring antimicrobial peptides, they
 CC are less likely to induce development of resistant strains

XX
 SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIP 3
 |||
 Db 1 RIP 3

RESULT 14

ADG13966
 ID ADC13966 standard; peptide; 4 AA.

XX
 AC ADC13966;

XX
 DT 18-DEC-2003 (first entry)

XX Rheumatoid arthritis antibody detecting peptide SEQ ID NO:91.

XX autoantibody; rheumatoid arthritis; citrulline.

XX Synthetic.

XX PN WO2003050542-A2.

XX PD 19-JUN-2003.

XX PF 11-DEC-2002; 2002WO-NL000815.

XX PR 11-DEC-2001; 2001NL-01019540.

XX PA (TEWE-) STICHTING TECH WETENSCHAPPEN.

XX PI Van Ventrooij WJM, Drijfhout JW, Van Boekel MAM, Pruijn GJM;

XX WPI; 2003-663235/62.

XX Detecting autoantibodies from patients suffering from rheumatoid
 PT arthritis, by contacting a reactive peptide comprising citrulline residue
 PT or its analog with autoantibodies to form a complex, and detecting the
 PT complex.

XX PS Claim 8; SEQ ID NO 91; 110pp; English.

XX The invention relates to a novel method for detecting autoantibodies from
 CC patients suffering from rheumatoid arthritis. The method involves
 CC contacting autoantibodies with at least one reactive peptide comprising a
 CC citrulline residue or its analogue for a time sufficiently long to allow
 CC a complex to be formed between the autoantibody and peptide, and
 CC detecting the complex. The present sequence represents a peptide of the
 CC invention.

XX SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 7; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IPR 4
 |||
 Db 2 IPR 4

RESULT 15

ADG94025

ID ADG94025 standard; peptide; 4 AA.

XX
 AC ADG94025;

XX
 DT 25-MAR-2004 (first entry)

XX Human JAM-1 permeabilising peptide SEQ ID NO:4.

XX human; permeabilising; interferon-beta; IFN-beta; mucosal delivery;
 KW immunosuppressive; virucide; autoimmune disease; viral disease;
 KW multiple sclerosis; chronic hepatitis B; condyloma acuminata;
 KW papilloma virus; childhood viral encephalitis; wart.

XX OS Homo sapiens.

XX PN WO2004002404-A2.

XX PD 08-JAN-2004.

XX PF 18-JUN-2003; 2003WO-US019261.

XX PR 28-JUN-2002; 2002US-0393066P.

XX PA (NAST-) NASTECH PHARM CO INC.

XX Quay SC, Gupta M, De Meireles JC, Abd El- Shafy M;

XX WPI; 2004-122360/12.

XX Stable pharmaceutical composition comprising interferon compound(s)
 PT formulated for mucosal delivery to mammalian subjects in combination with
 PT mucosal delivery-enhancing agent(s).

XX PS Disclosure; SEQ ID NO 4; 353pp; English.

XX The invention relates to a novel stable pharmaceutical composition
 CC comprising one or more interferon (IFN)-beta compound(s) formulated for
 CC mucosal delivery to a mammalian subject in combination with one or more
 CC mucosal delivery-enhancing agent(s), where the composition following
 CC mucosal administration to the subject yields enhanced mucosal delivery of
 CC the one or more IFN-beta compound(s). A composition of the invention has
 CC immunosuppressive and virucide activity. The composition is useful for
 CC treating autoimmune diseases, viral disease, for alleviating one or more
 CC symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma
 CC acuminata, papilloma virus warts of the larynx or skin or childhood viral
 CC encephalitis in the subject without unacceptable adverse side effects.
 CC The composition can be delivered intranasally which reduces or eliminates
 CC compliance problems and side effects that attend delivery by injection.
 CC The sequences shown in ADG94022-ADG94810 represent permeabilising
 CC peptides used in a composition of the invention.

XX SQ Sequence 4 AA;

Query Match 76.2%; Score 16; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIP 3
 |||
 Db 2 RIP 4

Search completed: June 20, 2005, 15:59:02
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